

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 15, 2005, 12:29:05 ; Search time 129 Seconds  
(without alignments)  
9576.067 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 2848  
Sequence: 1 ctcgagattacccttacag.....gaaataaattatctctgtgcc 1597

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/sgn2\_1/USPTO.spool\_p/US10775649/runat.14062005.141110.20646/app.query.fasta.1.1735  
-DB=A Geneseq 16Dec04 -QFMT=fasta -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10775649 @CGN 1.1 154 @runat.14062005.141110.20646 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT\_DSPLLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THRESHADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 16Dec04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1802	63.3	343	5	AB080277 Murine mu
2	1671	58.7	351	5	AB081134 Rat MURF1
3	1619.5	56.9	370	4	AA000918 Human bon
4	1613	56.6	353	4	AB050234 Human tra
5	1613	56.6	353	5	ABG93804 Human bon
6	1613	56.6	353	5	ADA55293 Human pro
7	1613	56.6	353	7	AD61549 Human pro
8	1613	56.6	353	7	AD61546 Human pro
9	1612.5	56.6	366	4	AAU15855 Human nov
10	1612.5	56.6	366	6	ABU54924 Human nov

11	1583.5	55.6	366	4	AAU25438 Human mod
12	1562	54.8	340	5	AB081135 Human MUR
13	1378	48.4	302	4	AA000998 Human bon
14	1126.5	39.6	452	6	AAE32110 Human cyt
15	1126.5	39.6	452	7	ADB64249 Human pro
16	1126.5	39.6	548	7	ADB64489 Human pro
17	1115	39.2	412	7	ADC31770 Human nov
18	1114.5	39.1	545	5	AB08275 Murine mu
19	1110	39.0	366	5	AB08275 Murine mu
20	1107	38.9	358	4	AAE32110 Human cyt
21	1107	38.9	358	4	AAE32110 Human cyt
22	1107	38.9	358	4	AAE32110 Human cyt
23	1103.5	38.7	396	3	AA021048 Human nuc
24	1073	37.7	201	5	AB081142 Rat MURF1
25	1070	37.6	400	5	AB081142 Human MUR
26	1015	35.6	289	5	AB081145 Human MUR
27	985	34.6	326	5	AB083475 Human cyt
28	979.5	34.4	414	4	AAU15868 Human nov
29	979.5	34.4	414	6	ABU54937 Human nov
30	886	31.1	254	4	AA061322 Human tra
31	846	29.7	602	8	ADP22642 Sea-squir
32	771.5	26.4	218	4	AA000805 Human bon
33	764	26.8	143	3	AA041076 Human ORF
34	764	26.8	143	5	ABP34078 Human int
35	676.5	23.8	181	7	ADC33320 Human nov
36	652.5	22.9	184	4	AAU16327 Human nov
37	652.5	22.9	184	6	ABU55396 Human nov
38	504	17.7	122	4	AAU16316 Human nov
39	504	17.7	122	6	ABU55385 Human nov
40	455	16.0	524	8	ADR09855 Human pro
41	436.5	15.3	736	7	ADM04867 Human pro
42	432.5	15.2	552	7	ADJ70562 Human hea
43	432.5	15.2	667	8	ADQ21458 Human sof
44	418.5	14.7	716	7	ADD01211 Human nuc
45	406.5	14.3	744	4	ABG18061 Novel hum

## ALIGNMENTS

RESULT 1

ABB08277  
ID ABB08277 standard; protein; 343 AA.

XX ABB08277;

XX DT 15-JUL-2002 (first entry)

XX DE Murine muscle ring finger protein 3 (MURF-3).

XX KW Muscle ring finger; MURF-3; mouse; cardiant; microtubule;  
intermediate filament; striated muscle; cardiac hypertrophy;  
heart disease.

XX OS Mus musculus.

XX PN WO200206318-A2.

XX PD 24-JAN-2002.

XX PF 18-JUL-2001; 2001WO-US022896.

XX PR 18-JUL-2000; 2000US-0219020P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX PI Olson EN, Spencer JA;

XX DR WPI; 2002-241506/29.

XX N-PSDB; ABA99063.

XX Novel muscle ring finger protein useful for drug screening, and for  
diagnosing and treating diseases, particularly cardiomyopathies.

PS Claim 3; Fig 10; 134pp; English.  
 XX The sequence represents murine muscle ring finger protein 3 (MURF-3). The  
 CC invention relates to a purified muscle ring finger (MURF) protein,  
 CC selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the  
 CC invention are involved in microtubule and intermediate filament  
 CC stabilisation of striated muscle cells and have cardiant activity. The  
 CC MURF proteins are useful for screening a candidate substance for MURF  
 CC protein-binding activity, in a cell, cell-free system or in vivo, and its  
 CC effect on interaction of MURF with microtubules, homodimerisation of  
 CC MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction  
 CC of MURF with intermediate filaments, e.g. desmin, vimentin and  
 CC cyokeratin, and heterodimerisation of MURF. The screened compounds are  
 CC useful for treating and preventing cardiac hypertrophy and heart  
 CC diseases. MURF proteins are useful as antigens to immunise animals for  
 CC the production of antibodies

XX SQ Sequence 343 AA;

Alignment Scores:  
 Pred. No.: 7 39e-147 Length: 343  
 Score: 1802.00 Matches: 343  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 63.27% Indels: 0  
 DB: 5 Gaps: 0

US-10-775-649-5 (1-1597) x ABB08277 (1-343)

QY 299 ATGGATTATAAATCTAGCCCTGATTCCTGATGGAACCTATGAGAACCTGGAGAACGAC 358  
 Db 1 MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20  
 QY 359 CTGATCTGCCCATCTGCCGAGAGTGTACCAAGCCTGTGTCATCTGCCCTGCCAA 418  
 Db 21 LeuileCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
 QY 419 CACAACCTCTGCCGGAAGTGTGCCAACGACATCTCCAGGCTCGAATCCCTACTCGACC 478  
 Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60  
 QY 479 AACCCGGTGGCTCAGTGTCCATGTCTCGAGGTGCTTCCGTTGCCCTCGTCCGCCAT 538  
 Db 61 AsnArgGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80  
 QY 539 GAAGTATCATGACCGGACCGGGGTGTACGGCTCGAGGACCTGCTGTGGAAAC 598  
 Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100  
 QY 599 ATCATTGACATCTACAAGCAGGAGTGTCCAGTCGGCCCTCGAGAAAGCAGCCACCG 658  
 Db 101 IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120  
 QY 659 ATGTCAAGGAACACAGAACGAGAGATCAACATCTACTGTCTCAGTGTGAGTGCCT 718  
 Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
 QY 719 ACTTGCTCTCTGTGCAAGGTGTTGGGCTCACCAGCCCTGTCAGGTGCCCCCTTGCAA 778  
 Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
 QY 779 AGCATCTTCAAGACAGAGACTGAGCTGAGTGAATCTGTCATCTCCATCTGCTGGTGGGG 838  
 Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
 QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGAG 898  
 Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
 QY 899 AATAGCCACGAGTGAAGGAGGCTGACTCAGAGTTTGACACCTCTACGCCATCTCG 958  
 Db 201 AsnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220

QY 959 GATGAGAAGAAGAGAGAGCTGCTGCAGCGGATCACGACGAGCAGGAGAGAGCTGGGC 1018  
 Db 221 AspGluLysLysSerGluLeuLeuGlnAlaGlyIleThrGlnGlnGlnGluLysLeuGly 240  
 QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078  
 Db 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260  
 QY 1079 GAGACCGCCATCCAGTCCCTGATGAGCCGCGAGGGCTACCTTCCTCAAGTGCACAG 1138  
 Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys 280  
 QY 1139 CAGCTCATCAAGAGCATCTAGAACCTCCAAAGGCTGCAGCTGGGGAAGACAGACAA 1198  
 Db 281 GlnLeuLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
 QY 1199 GGCTTTGAGAACATGGACTACTTTACTTGGACTTAGAACACATACAGAGCGCTTGAGG 1258  
 Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320  
 QY 1259 GCCATTGACTTTGGACACAGTAAAGATGCTGATGTACATGTTGACCTTTGAAGGCAG 1318  
 Db 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340  
 QY 1319 CGTTCCTCT 1327  
 Db 341 ArgSerSer 343  
 RESULT 2  
 ABB81134  
 ID ABB81134 standard; protein; 351 AA.  
 XX AC ABB81134;  
 XX DT 05-NOV-2002 (first entry)  
 XX DE Rat MURF1 protein.  
 XX KW Muscle atrophy protein; MURF1; MURF3; MAFB3; atrophy; neuroprotective;  
 XX OS Rattus sp.  
 XX PN WO200261046-A2.  
 XX PD 08-AUG-2002.  
 XX PF 30-JAN-2002; 2002WO-US002811.  
 XX PR 30-JAN-2001; 2001US-0264926P.  
 XX PR 10-AUG-2001; 2001US-0311697P.  
 XX PR 22-OCT-2001; 2001US-0338742P.  
 XX PA (REGE-) REGENERON PHARM INC.  
 XX PI Glass DJ, Bodine SC;  
 XX DR WPI; 2002-608513/65.  
 XX DR N-PSDB; ABQ79506.  
 XX PT Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g.  
 XX PT MURF1, MURF3 or MAFB3, useful for treating muscle atrophy and other  
 XX PT related disorders, e.g. Guillian-Barre syndrome, peripheral neuropathy,  
 XX PT and nerve damage.  
 XX PS Claim 1; Fig 7; 104pp; English.  
 XX CC The invention relates to isolated nucleic acid molecules encoding muscle  
 XX CC atrophy proteins MURF1, MURF3, or MAFB3. The proteins can be expressed by  
 XX CC standard recombinant methodology. The nucleic acid molecules and  
 XX CC polypeptides are useful for treating muscle atrophy or detecting atrophy,  
 XX CC and for treating related diseases/disorders, e.g. Guillian-Barre  
 XX CC syndrome, peripheral neuropathy, or nerve damage caused by environmental

CC toxins or drugs. The MURF1, MURF3 and MAFB antagonists, and the  
CC antagonists of their pathways are useful for inhibiting atrophy, inducing  
CC hypertrophy, decreasing ubiquitination, interfering with the ubiquitin  
CC pathway, or modulating MURF1, MURF3 or MAFB expression or activity. The  
CC nucleotide sequences are useful for diagnostic and genetic testing. The  
CC present sequence represents a rat MURF1 protein  
XX  
SQ Sequence 351 AA;

Alignment Scores:  
Pred. No.: 1,67e-135 Length: 351  
Score: 1671.00 Matches: 319  
Percent Similarity: 98.18% Conservative: 1  
Best Local Similarity: 97.85% Mismatches: 6  
Query Match: 58.67% Indels: 0  
DB: 5 Gaps: 0

US-10-775-649-5 (1-1597) x ABB81134 (1-351)

Qy 299 ATGGATTATAATCTAGCTGATCTCTGATGAAACGCTATGAGAACCTGGAGAACGAG 358  
Db 1 MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20  
Qy 359 CTGATCTGCCCATCTGCTGGAGATGTTACCAAGCCTGTGCTCATCTGCCCTGCCAA 418  
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40  
Qy 419 CACAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGACCC 478  
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60  
Qy 479 AACCCGGTGGCTAGTGTCCATGTCTGGAGTCTGTCGCTGCTTCCGTTGCCCTGTCGCCCAT 538  
Db 61 AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80  
Qy 539 GAAGTGATCATGGACCGGACCGGCTGTACGCCCTGCAGAGCAACCTGCTGTGGAAC 598  
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100  
Qy 599 ATCATTTGACATCTACAAGCAGAGAGTCTCCAGTCCGGCCCTGCAGAAAGGACGACCCG 658  
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120  
Qy 659 ATGTCCAGGACACAGAACGAGAGATCAACATCTACTGTCTCAGCTGTGAGTGTGCT 718  
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
Qy 719 ACTTCTCTTGTGCAAGGTGTTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCCAA 778  
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
Qy 779 AGCATCTTCCAGGACAGAGACTGAGTGTAGTAACTGCATCTCCATGTGTGCGCGGG 838  
Db 161 SerIlePheGlnGlyValLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
Qy 839 AACGACCGAGTGCAGACCATCTCTCAGCTGGAGGACTCGTCAGAGTGCACCAAGAG 898  
Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
Qy 899 ATAGCCACCGTGCAGAGGAGCTGAGTCAAGATTTGACACCTCTACGCCATCTGTG 958  
Db 201 AsnSerHisGlnValLysGluGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220  
Qy 959 GATGAGAAGACGAGCTGTGCGCGGATCAACGAGGACGAGGAGAGTGGGC 1018  
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuAsp 240  
Qy 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078  
Db 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuLysSerThrLysLeuVal 260  
Qy 1079 GAGACCGCATCCAGTCCCTGATGAGCCGCGGAGGGCTACCTTCTCTCAAGTCCCAAG 1138

Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280  
Qy 1139 CAGCTCATCAAGAGCATTGTAGAAGCCCTCAAGGCTGCCAGCTGGGAAGACAGACAA 1198  
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
Qy 1199 GCGTTTGAGAACATGGACTACTTACTCTGACTTAGAACACATAGCAGGCGCTTGAGG 1258  
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320  
Qy 1259 GCCATTGACTTTGGGACA 1276  
Db 321 AlaIleAspPheGlyThr 326  
RESULT 3  
AAM00918  
ID AAM00918 standard; protein; 370 AA.  
XX  
AC AAM00918;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human bone marrow protein, SEQ ID NO: 394.  
XX  
KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;  
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;  
KW immunosuppressive; gene therapy; cytokine cell proliferation;  
KW cell differentiation modulator; immune disorder; infection; cancer;  
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153453-A2.  
XX  
PD 26-JUL-2001.  
XX  
PF 23-DEC-2000; 2000WO-US034960.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 30-NOV-2000; 2000US-0250583p.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;  
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Drmanac RT;  
XX  
DR WPI; 2001-488707/53.  
DR N-PSDB; AAH90037.  
XX  
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful for  
PT treating e.g. cancer and immune deficiency disorders.  
XX  
PS Claim 10; Page 481-482; 648pp; English.  
XX  
CC The present sequence is one of 251 novel human polypeptides encoded by a  
CC bone marrow-expressed polynucleotide. The polynucleotide and the  
CC polypeptide encoded by it are useful in the treatment of various immune  
CC deficiencies and disorders. The deficiencies and disorders may be  
CC genetic, may be caused by a viral (e.g. HIV), bacterial or fungal  
CC infection, or may result from an autoimmune disorder, a coagulation  
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,  
CC suppression of an inflammatory response or treatment of a nervous system  
CC disorder such as Alzheimer's disease. Detection of the presence or  
CC increased expression of the polynucleotide or the protein it encodes is  
CC useful for the diagnosis and/or prognosis of one or more types of cancer.

CC The polynucleotide and polypeptide can be used as nutritional sources or  
XX supplements and in the screening of chemical compounds as potential drugs  
SQ Sequence 370 AA;

Alignment Scores:  
Pred. No.: 4.95e-131 Length: 370  
Score: 1619.50 Matches: 309  
Percent Similarity: 94.48% Conservative: 16  
Best Local Similarity: 89.83% Mismatches: 14  
Query Match: 56.86% Indels: 5  
DB: 4 Gaps: 1

US-10-775-649-5 (1-1597) x AAM00918 (1-370)

QY	245	AGCAAGAGCTTGGTGTGACGAGGTGGGCAAGACAGTGCATTTCAAGCAATATGGAT	304
DB	1	ArgArgGlnLeuGlyValAlaLeuIlePro- - - - -SerHisArgMetAsp	15
QY	305	TATAATCTAGCTGATTCCTGATGAACGCTATGAGAACCTGGAGAGCAGCTGATC	364
DB	16	TyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluysGlnLeuIle	35
QY	365	TGCCCCATCTGCTGGAGATGTTTACCAAGCCCTGTGTCATCTCCCTGCCCAACAAC	424
DB	36	CysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGlnHisAsn	55
QY	425	CTCTGCGGAGTGTGCCACGACATCTCCAGGCTGCGATCCCTACTGGACCAACGC	484
DB	56	LeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThrSerArg	75
QY	485	GGTGGCTCAGTGTCCATGTCTGAGGTGCTTCCGTTGCGCCGCGCCATGAAGTG	544
DB	76	GlySerSerValSerMetSerGlyLysArgPheArgCysProThrCysArgHisGluVal	95
QY	545	ATCATGACGGCACGGGGTGTACGCCCTGCAGAGAACCTGCTGTGGAAACATCAT	604
DB	96	IleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsnIleIle	115
QY	605	GACATCTACAGCAGAGTGTCTCCAGTCCGCGCCCTGCAGAAAGCCACCCGATGTC	664
DB	116	AspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisProMetCys	135
QY	665	AAGCAACACGAACAGAGATCAACATCTACTGTCTCAGGTGAGGTGCTTACTTGC	724
DB	136	LysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValProThrCys	155
QY	725	TCCTTGTCAAGGTGTTTGGGGCTCACCGGCTGTGAGGTGCCCTTTGCAAGCATC	784
DB	156	SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal	175
QY	785	TTCCAGGACAGAGACTGAGTGAAGTCACTCCATCTCCATGCTGGTGGGGGACGAC	844
DB	176	PheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGlyAsnAsp	195
QY	845	CGAGTGCACAGCATCTCTCAGCTGGAGGACTCGTGACAGTGCACCAAGAGATAGC	904
DB	196	ArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGluAsnSer	215
QY	905	CACAGGTGAAGAGGAGTGTAGTCAAGATTGTGACACCTCTACCCCATCTGGATGAG	964
DB	216	HisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeuAspGlu	235
QY	965	AGAAAGCGAGTGTGAGCGGATCAGCGAGGACGAGAGAGTGGGCTTCATC	1024
DB	236	LysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSerPheIle	255
QY	1025	GAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTTGGAGAC	1084
DB	256	GluAlaLeuIleGlnGlnTyrGlnGluGlnLeuAspLysSerThrLysLeuValGluThr	275
QY	1085	GCCATCCAGTCCCTGATGAGCCCGAGGGGTACCTTCTCTCAAGTCCCAAGCAGCTC	1144

DB	276	AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLysGlnLeu	295
QY	1145	ATCAAGAGCATTTGTAAGCCTCCAGGGCTGCCAGCTGGGGAAGACAGAGCGCTTT	1204
DB	296	IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGlnGlyPhe	315
QY	1205	GAGAACATCGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGGGGCCAT	1264
DB	316	GluAsnMetAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle	335
QY	1265	GACTTTGGGACA	1276
DB	336	AspPheGlyThr	339
RESULT 4			
ABB50234	ID ABB50234 standard; protein; 353 AA.		
XX	ABB50234;		
XX	05-FEB-2002 (first entry)		
DT	Human transcription factor TRFX-85.		
XX	Human; transcription factor; TRFX; cell proliferative disease;		
KW	autoimmune disease; inflammation; neurological disease;		
KW	developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;		
KW	neuroprotective; antiinflammatory; gene therapy.		
XX	Homo sapiens.		
XX	WO200172777-A2.		
XX	04-OCT-2001.		
XX	13-MAR-2001; 2001WO-US008117.		
XX	13-MAR-2000; 2000US-0189986P.		
PR	(INCY-) INCYTE GENOMICS INC.		
PA	Hillman JL, Baughn MR, Yue H, Lal P, Lu DAM, Patterson C;		
XX	Azimzai Y, Bandman O, Tang YT, Mathur P, Shah P, Au-Young J;		
PI	Reddy R;		
XX	WPI; 2001-570896/64.		
DR	N-PSDB; ABA83058.		
XX	Novel transcription factor polypeptides, used to treat diseases		
PT	associated with altered activity and expression of TRFX, and to screen		
PT	for agents capable of modulating its activity.		
XX	Claim 1; Page 227-228; 327pp; English.		
PS	The present sequence is the protein sequence for a human transcription		
XX	factor. The transcription factor and its coding sequence are useful in		
CC	the diagnosis, treatment and prevention of diseases associated with		
CC	altered expression of the transcription factor e.g. cell proliferative,		
CC	autoimmune/inflammatory, neurological and developmental disorders. A		
CC	number of specific disorders/diseases are given in the specification,		
CC	including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,		
CC	allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic		
CC	dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,		
CC	Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,		
CC	psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative		
CC	colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's		
CC	disease, stroke, and viral, bacterial, fungal and protozoal infections		
XX	Sequence 353 AA;		
SQ	Alignment Scores:		
Pred. No.:		1.77e-130	Length: 353
Score:		1613.00	Matches: 305



299	ATGGATTATAAATCTAGCCTGATTCCTGATGGAACCGCTATGGAGAACTTGAGAGACGAG	Qy
358	MetAspTyrLysSerSerLeuIleGlnAspGlyAenProMetGluAaenLeuGluLysGln	Db
1	MetAspTyrLysSerSerLeuIleGlnAspGlyAenProMetGluAaenLeuGluLysGln	20
359	CTGATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCTGTGGTCATCTCGCCCTGCCAA	Qy
418	LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln	40
21	LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln	40
419	CACAACTCTCCGGAGTGTGCCAACGACATCTTCCAGGGTGCGAATCCCTTACTGGACC	Qy
478	HisAenLeuCysArgLysCysAlaAaenAspIlePheGlnAlaAaenProTyrTrpThr	60
41	HisAenLeuCysArgLysCysAlaAaenAspIlePheGlnAlaAaenProTyrTrpThr	60
479	AACCGCGTGGCTCAGTGTCATGTCTGGAGGTGGTTTCGGTTGGCCCTCTGTCGCCGCAT	Qy
538	SerArgGlySerSerValSerMetSerGlyArgPheArgCysProThrCysArgHis	80
61	SerArgGlySerSerValSerMetSerGlyArgPheArgCysProThrCysArgHis	80

QY 539 GAAGTGATCATGACCGGACGGGGTGTACGGCTCGAGAGAACCTGTGTGGAAAC 598  
 Db |||||  
 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100  
 QY 599 ATCATTGACATCTACAGCAGAGTGTCTCAGTCGGCCCTCGAGAAAGCAGCCCG 658  
 Db |||||  
 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120  
 QY 659 ATGTGCAAGGACACCAAGCAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCT 718  
 Db |||||  
 121 MetCysLysGlnHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
 QY 719 ACTTGCTCTCTGTGCAAGGTGTTGGGGCTCACAGCGCTGTGAGGTGCCCTTTGCAA 778  
 Db |||||  
 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160  
 QY 779 AGCATCTTCAGGACAGAGCTGAGTGAATCTGATCTCCATCTCAGTGTGTGGGGGG 838  
 Db |||||  
 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180  
 QY 839 AACGACCGAGTGCAGAGTCTCTCTCAGCTGGAGGACTCGTCAGAGTGCACAGGAG 898  
 Db |||||  
 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGlu 200  
 QY 899 AATAGCCACCGAGTGAAGGAGGAGCTGAGTCAAGATTTCACACCTCTACGCCATCTCG 958  
 Db |||||  
 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220  
 QY 959 GATGAGAAGACGAGCTGTGCGAGCGGATCACGAGGAGCAGAGAGCTGGGC 1018  
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 QY 1019 TTCATCGAGCTCTGATCTCCAGTACAGGAGCAGCTGMAAGTCCACCAAGCTGTG 1078  
 Db |||||  
 241 PheIleGluAlaLeuIleGlnTyrGlnGlnLeuAspLysSerThrLysLeuVal 260  
 QY 1079 GAGACCGCCATCCAGTCCCTGATGAGCCGGAGGGCTACCTTCTCAAGTGCACAG 1138  
 Db |||||  
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 QY 1139 CAGCTCATCAAGACATTTGTAGAGCTCCAGGGCTGCGAGTGGGGAGACAGACAA 1198  
 Db |||||  
 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
 QY 1199 GGTCTTTGACACATGACTACTTTACTCTGGACTTAGAACACATAGCAGCGCTTGAGG 1258  
 Db |||||  
 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320  
 QY 1259 GCCATTGACTTTGGGACA 1276  
 Db |||||  
 321 AlaIleAspPheGlyThr 326  
 RESULT 6  
 ADA55293  
 ID ADA55293 standard; protein; 353 AA.  
 XX  
 AC  
 AC ADA55293;  
 XX  
 DT 20-NOV-2003 (first entry)  
 DE  
 DE Human protein, SEQ ID 2861.  
 XX  
 KW Cytotoxic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
 KW inflammatory disease; osteoporosis; neurological disease.  
 XX  
 OS Homo sapiens.  
 PN  
 PN EP1293569-A2.  
 XX  
 PD 19-MAR-2003.  
 XX  
 PF 21-MAR-2002; 2002EP-00006586.

XX  
 PR 14-SEP-2001; 2001JP-00328381.  
 PR 24-JAN-2002; 2002US-0350435P.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Naganari K, Masuho Y;  
 XX  
 DR WPI; 2003-395539/38.  
 DR N-PSDB; ADA53654.  
 XX  
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 PT which the gene is involved, or as target molecules for gene therapy.  
 XX  
 PS Claim 14; SEQ ID NO 2861; 205pp; English.  
 XX  
 CC The present invention relates to novel human secretory or membrane  
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
 CC ADA54071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.  
 XX  
 SQ Sequence 353 AA;  
 Alignment Scores:  
 Pred. No.: 1,77e-130 Length: 353  
 Score: 1613.00 Matches: 305  
 Percent Similarity: 97.55% Conservative: 13  
 Best Local Similarity: 93.56% Mismatches: 8  
 Query Match: 56.64% Indels: 0  
 DB: Gaps: 6  
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 QY 299 ATGGATTATAATCTAGCCTGATTCCTGATGAAACGCTATCGAGAACCTGGAGAGCAG 358  
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 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20  
 QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTATCTCGCTCCCAA 418  
 Db |||||  
 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
 QY 419 CACACCTCTCGCGGAGTGTCCCAACAGACATCTCCAGGCTCGCAATCCCTACTCGACC 478  
 Db |||||  
 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60  
 QY 479 AACCGGGTGGCTCAGTGTCCATGTCTGAGGTCTGTTCCGTTGCCCTCGCGCCCAT 538  
 Db |||||  
 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80  
 QY 539 GAAGTGATCATGACCGGACCGGGTGTACGGCTCGAGAGAACCTGTGTGGAAAC 598  
 Db |||||  
 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100  
 QY 599 ATCATTGACATCTACAGCAGAGTGTCTCAGTCGGCCCTCGAGAAAGCAGCCCG 658  
 Db |||||  
 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120  
 QY 659 ATGTGCAAGGACACCAAGCAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCT 718  
 Db |||||  
 121 MetCysLysGlnHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
 QY 719 ACTTGCTCTCTGTGCAAGGTGTTGGGGCTCACAGCGCTGTGAGGTGCCCTTTGCAA 778  
 Db |||||  
 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160  
 QY 779 AGCATCTTCAGGACAGAGCTGAGTGAATCTGATCTCCATCTCAGTGTGTGGGGGG 838  
 Db |||||  
 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180

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QY 839 AACGCCAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGAGAGTGCACCAAGGAG 898
DB 161 AenAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGlu 200
QY 899 AATAGCCACCGTGAAGGAGGAGTGTAGTCAGAGTTTGACACCTCTAGCCATCTTG 958
DB 201 AenSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGACGAGCGAGTGTCTGAGCGGATCACGACGAGGAGGAGGAGTGGCG 1018
DB 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSer 240
QY 1019 TTCATCGAGGCTCTCATCTCCAGTACAGGAGGAGCTGGAAAGTCCACCAAGTTGTG 1078
DB 241 PheIleGluAlaLeuIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 260
QY 1079 GAGACGGCATCCAGTCCCTGATGAGCGGAGGAGGAGTCTCTCTCAAGTGGCCAG 1138
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGCAGCATTTAGAACCTCCAGGCTCCAGCTGGGAGACAGACAA 1198
DB 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGln 300
QY 1199 GCGTTTGAGAACATGAGTACTTTACTCTGGACTTAGAACACATAGCAGGCGCTTGAGG 1258
DB 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTGGGACA 1276
DB 321 AlaIleAspPheGlyThr 326
RESULT 7
ADE61549
ID ADE61549 standard; protein; 353 AA.
AC ADE61549;
DT 29-JAN-2004 (first entry)
DE Human Protein Q969Q1, SEQ ID NO 7469.
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS WO2003016475-A2.
PN 27-FEB-2003.
PD 14-AUG-2002; 2002WO-US025765.
PP 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
CC
```

```
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 353 AA;
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Alignment Scores:
Pred. No.: 1,77e-130 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 7 Gaps: 0
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US-10-775-649-5 (1-1597) x ADE61549 (1-353)

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DB 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCCATCTGCTGAGATGTTTACCAAGCTGTGGTCTATCTGCTCCCTGCCNA 418
DB 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
QY 419 CACACCTCTGCGGAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTGGCGCCAT 538
DB 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGACCGGCACGGGTGTACGGCTGCGAGAGAACCTGCTGTGTGAAAC 598
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTCTCCAGTGGCCCTTCAGAAAGGAGCCACCCG 658
DB 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTCAAGGAACACGAGAGACGAGAGATCAACTACTGTCTACGTGTGAGGTGCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTTGTGCAAGGTGTTTGGGCTACACAGGCTGTGAGGTGCCCTTTGCCAA 778
DB 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGACAGACTGAGTGAAGTAACTCATCTCATCTGCTGTGAGGTGCT 838
DB 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
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QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGCGAGAGTGACCAAGGAG 898
DB 181 AAspArgValGlnThrIleThrGlnLeuGluAspSerArgValThrLysGlu 200
QY 899 AATAGCCACGAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCCTG 958
DB 201 AsnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAGGAGGAGCGAGCTGCTGCAGCGGATCACCGAGGAGGAGGAGCTGGGC 1018
DB 221 AspGluLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSer 240
QY 1019 TTCTATCGAGGCTCTGATCTCTCCAGTACAGGAGCAGCTGAAAGTCCACCAAGCTTGTG 1078
DB 241 PheIleGluAlaLeuLeuGlnGlnTyGlnGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACGCCATCCAGTCCCTCGATAGAGCCCGGAGGGCTACCTCTCTCAAGTGCCAAAG 1138
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAGAGCATTTGAGAGCTCCAGAGCTGCCAGGCTGCCAGTGGGAGACAGACAA 1198
DB 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATACAGAGGCTTGAGG 1258
DB 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
DB 321 AlaIleAspPheGlyThr 326
RESULT 8
ADE61546
ID ADE61546 standard; protein; 353 AA.
XX
AC ADE61546;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q969Q1, SEQ ID NO 7466.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
```

```
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 353 AA;
```

```
Alignment Scores:
Pred. No.: 1.77e-130 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 7 Gaps: 0
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US-10-775-649-5 (1-1597) x ADE61546 (1-353)

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QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTCATCTCGCCTGCCAA 418
DB 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTCTCGCGAAGTGTCCCAACGACATCTTCCAGGCTCGCAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTprThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCGAGGTGCTTCCGTTGCCCTCGTCGCGCCAT 538
DB 61 SerArgLysSerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGGACCGGCACCGGGTGTACGGCTGTGACAGGAAACCTGTGTGGAAAC 598
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100
QY 599 ATCATTGACATCTACAGCAGGAGTGTCTCCAGTGGCCCTCGAGAAAGCGACGCCG 658
DB 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGAACAGACGAGAGATCAACATCTACTGTCTACGTGTGAGGTGCCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTTGCAAGGTGTTTGGGGCTCACCGGCTGTGAGGTTCCTCCCTTTGCAA 778
DB 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAAGTATCTCCATCTGCTGTGGCGGG 838
DB 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
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PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-488783/53.  
XX N-PSDB; AAS25842.  
XX  
XX New nucleic acid molecules encoding 461 human secreted proteins for  
XX diagnosing, preventing, treating or ameliorating medical conditions and  
XX used as food additives or preservatives.  
XX  
XX Claim 11; SEQ ID NO 808; 980pp; English.  
XX  
XX The invention relates to isolated nucleic acid molecules and their  
XX encoded secreted proteins. The nucleic acids and proteins are used to  
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
XX in diagnosing a pathological condition or susceptibility to a  
XX pathological condition. Antibodies to the proteins can also be used in  
XX alleviating symptoms associated with the disorders and in diagnostic  
XX immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
CC and many other disorders listed in the specification. The polypeptides  
CC can also be used to aid wound healing and epithelial cell proliferation,  
CC to prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence represents a novel secreted protein of the invention. Note: The  
CC sequence data for this patent did not form part of the printed

Alignment Scores:  
Pred. No.: 1.99e-130 Length: 366  
Score: 1612.50 Matches: 308  
Percent Similarity: 94.19% Conservative: 16  
Best Local Similarity: 89.53% Mismatches: 15  
Query Match: 56.62% Indels: 5  
DB: 4 Gaps: 1

US-10-775-649-5 (1-1597) x AAU15855 (1-366)

QY 245 AGACAAGACTTGGTGTGACGAGGTGGCGACAGACAGTCGCATTTCAAGCAATATGGAT 304  
DB 1 ArgArgGlnLeuGlyValAlaLeuIlePro-----SerHisArgMetAsp 15  
QY 305 TATAAATCTAGCTGATTCCTGATGGAACGCTATGAGAACTGAGAGAACTGAGAGAGAGCTGATC 364  
DB 16 TyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGlyGlnLeuIle 35  
QY 365 TCCCCATCTGCTGGAGATGTTTACCAAGCTGTGGTTCATCTGCGCTCCCTGCCAACCAAC 424  
DB 36 CysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGlnHisAsn 55  
QY 425 CTCTCCGGAAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCCG 484  
DB 56 LeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThrSerArg 75  
QY 485 GGTGGCTCAGTCTCCAGTCTGAGGTCTTCCGTTGCTGCTGCGCGCCATGAAGTG 544  
DB 76 GlySerSerValSerMetSerGlyArgPheArgCysProThrCysArgHisGluVal 95  
QY 545 ATCATGGACCGCAGCGGGGTGTACGGCTGTGACAGAGAACTGCTGTGTGAAACATCATTT 604  
DB 96 IleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsnIleIle 115  
QY 605 GACATCTACAAGCAGGAGTCTCCAGTGGCGCCCTGCAGAAAGGCGACCCGATGTGC 664  
DB 116 AspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisProMetCys 135  
QY 665 AAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTCACGTGTGAGGTGCTTACTTGC 724  
DB 136 LysGluHisGluAspGluLysAsnAsnIleTyrCysLeuThrCysGluValProThrCys 155  
QY 725 TCCTTGTGCAAGGTGTTTGGGGCTCACAGGCTGTGAGGTGGCCCTTTGCAAGCATC 784  
DB 156 SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal 175  
QY 785 TTCCAAGGACAGACAGCTGAGTCTCACTCTCCATCTCCATCTGCTGCGGGGACGAC 844  
DB 176 PheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGlyAsnAsp 195  
QY 845 CGAGTCGACACCATCATCTCTCAGCTGGAGGAGTCTGTCAGAGTGCACCAAGAGATAGC 904  
DB 196 ArgValGlnThrIleIleThrGlnLeuGluAspSerArgArgValThrLysGluAsnSer 215  
QY 905 CACCAAGTGAAGAGAGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCTGGATGAG 964

Db 216 HisGlnValLeuGluLeuSerGlnLysPheAspThrLeuTyraIleLeuAspGlu 235  
QY 965 AAGAAGAGCGACTGTCAGCGGATCAAGCAGGAGCAGGAGCAAGCTGGCTTCATC 1024  
Db 236 LysLysSerGluLeuGlnArgIleThrGlnGluGlnLysLeuSerPheIle 255  
QY 1025 GAGGCTCTGATCCTCAGTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGAGACC 1084  
Db 256 GluAlaLeuIleGlnGlnTyrglnGlnLeuAspLysSerThrLysLeuValGluThr 275  
QY 1085 GCATCCAGTCCCTGGATGAGCCCGAGGGGCTACTCTCTCAAGTGCCACGAGCTC 1144  
Db 276 AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuThrAlaLysGlnLeu 295  
QY 1145 ATCAAGAGCATTTAGAACCTCCAGGCTGCCAGCTGGGGAAGACAGACAAAGCTTT 1204  
Db 296 IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGlnGlyPhe 315  
QY 1205 GAGACATGGACTACTTACTCTGACTTAGAACACATAGACAGAGCCTTGAGGCCATT 1264  
Db 316 GluAenMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle 335  
QY 1265 GACTTTGGGACA 1276  
Db 336 AspPheGlyThr 339  
RESULT 10  
ID ABUS4924  
XX ABUS4924 standard; protein; 366 AA.  
AC ABUS4924;  
XX  
DT 18-MAR-2003 (first entry)  
XX  
DE Human novel polypeptide #11.  
XX  
KW Human; neural disorder; immune system disorder; renal disorder;  
KW muscular disorder; respiratory disease; reproductive disorder;  
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;  
KW hyperproliferative disorder; inflammatory disease; allergic reaction;  
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;  
KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;  
KW haemostatic; antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX  
PN US2002132753-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 17-JAN-2001; 2001US-00764864.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 07-JUL-2000; 2000US-0216547P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 14-AUG-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 22-AUG-2000; 2000US-0225868P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
XX  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
XX (BARA/) BARASH S C.  
PI Rosen CA, Ruben SM, Barash SC;  
XX  
DR WPI; 2003-147444/14.  
DR N-PSDB; ABX73183.  
XX  
PT New polypeptides and nucleic acids, useful in gene therapy for treating,  
PT inhibiting or preventing e.g. neural, immune system, muscular,  
PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or  
PT renal disorders.  
XX  
PS Claim 11; SEQ ID NO 808; 402pp; English.  
XX  
CC The invention relates to human novel polypeptides and their associated  
CC polynucleotides. The polypeptides and polynucleotides are useful in gene  
CC therapy for treating, inhibiting or preventing neural disorders, immune  
CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis  
CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.  
CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left  
CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage  
CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and  
CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and  
CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
CC related disorders (e.g. thrombosis, atherosclerosis and myocardial  
CC infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and  
CC ABUS5748 represent human novel polypeptides of the invention  
XX  
SQ Sequence 366 AA;  
Alignment Scores:  
Pred. No.: 1.99e-130 Length: 366  
Score: 1612.50 Matches: 308  
Percent Similarity: 94.19% Conservative: 16  
Best Local Similarity: 89.53% Mismatches: 15  
Query Match: 56.62% Indels: 5  
DB: 6 Gaps: 1  
US-10-775-649-5 (1-1597) x ABUS4924 (1-366)





DB:	4	Gaps:	1
US-10-775-649-S (1-1597) x AAU25438 (1-366)			
QY	245	AGACAAAGACTTGGTGTGACGACGCTGGCGCAAGACAGTGCATTTCAAAGCAATATTCGAT	304
Db	1	ArgargGlnLeuGlyValAlaLeuLeuPro-----SerHisArgMetAsp	15
QY	305	TATAAATCTAGCCTGATTCTCTGATGGAAACGCTATGAGAACCTCGGAGAACGACCTGATC	364
Db	16	TyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGlnLeuIle	35
QY	365	TGCCCCATCGCTGGAGATGTTTACCAAGCCTGTGTATCCTCGCTCGCTGCTGCAACAAC	424
Db	36	CysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGlnHisAsn	55
QY	425	CTCTGCCGGAAGTGTGCAACGACATCTCCAGAGCTCGAATCCTACTCGAACCAACCGC	484
Db	56	LeuCysargLysCysAlaAsnAspIlePheGlnAlaSerAsnProTyrLeuProThrArg	75
QY	485	GGTGGCTCAGTGTCCATGTCGTGGAGGTGCTTTCCGTTGCCCTCGTCCGCCCATGAAGTG	544
Db	76	GlyGlyThrThrMetAlaSerGlyLysArgPheargCysProSerCysArgHisGluVal	95
QY	545	ATCATGACCGGCACGGGGTGTACGGCTGCAGAGGAACCTGCTGGTGGGAAACATCATTT	604
Db	96	ValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleIle	115
QY	605	GACATCTACAGCAGGAGTGTCTCAGTCCGCGCCCTGCAGAAAGCAGCCACCCGATGTC	664
Db	116	AspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisProMetCys	135
QY	665	AAGGAAACCAAGAACGAGAACATCAAATCTACTGTCTCAGTGTGAGGTGCCTTACTTGC	724
Db	136	LysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValProThrCys	155
QY	725	TCCTTTGTCAAGGTGTTTGGGGCTCACAGGCGCTGTGAGGTGGCCCTTTGCAAAAGCATC	784
Db	156	SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal	175
QY	785	TTTCAAGGACAGAGACTGAGCTCAGTAACGTATCTCCATGCTGGTGGGGGGAACGAC	844
Db	176	PheGlnGlyLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGlyAsnAsp	195
QY	845	CGAGTCGACAGCATCATCTCTCAGCTGGAGGACTCGTCGACAGTGCACCAAGGAGATAGC	904
Db	196	ArgValGlnThrIleIleThrGlnLeuGluAspSerArgArgValThrLysGluAsnSer	215
QY	905	CACAGGTGAAGGAGGAGCTGAGTCAGAGTTTGACACCTCTACGCCATCCTGGATGAG	964
Db	216	HisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeuAspGlu	235
QY	965	AAGAAGACCGAGCTGCTGCAGCGGATCACGAGGAGCAGGAGGAGAGCTGGGCTTCATC	1024
Db	236	LysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLysLeuSerPheIle	255
QY	1025	GAGGCTCTGATCTCCAGTACAGGAGGAGCTGCAAAAGTCCACCAAGCTGTGGAGACC	1084
Db	256	GluAlaLeuIleGlnGlnTyrGlnGlnLeuAspLysSerThrLysLeuValGluThr	275
QY	1085	GCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCTTCCTCAAGTGCCACAGAGCTC	1144
Db	276	AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLysGlnLeu	295
QY	1145	ATCAAGAGCATTTAGAGCCTCCAGGGCTGCCAGCTGGGGGAGACAGAGCAGGCTTT	1204
Db	296	IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGlnGlyPhe	315
QY	1205	GAGAACATGGACTACTTTTACTCTGGACTTAGAACAACATAGCAGAGCGCTTCGAGGCCATT	1264
Db	316	GluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle	335
QY	1265	GACTTTGGGACA	1276

Db		336 AspPheGlyThr 339
ABB81135		
RESULT 12		
ID	ABB81135	standard; protein; 340 AA.
AC	ABB81135;	
XX	05-NOV-2002	(first entry)
XX	Human MURF1	protein.
XX	Muscle atrophy protein; MURF1; MURF3; MAFBX;	atrophy; neuroprotective;
KW	gene therapy; transgenic; human.	
XX	Homo sapiens.	
XX	W0200261046-A2.	
XX	08-AUG-2002.	
XX	30-JAN-2002;	2002WO-US002811.
XX	30-JAN-2001;	2001US-0264926P.
PR	10-AUG-2001;	2001US-0311697P.
PR	22-OCT-2001;	2001US-0338742P.
XX	(REGE-)	REGENERON PHARM INC.
XX	Glass DJ,	Bodine SC;
XX	WPI;	2002-608513/65.
DR	N-PSDB;	ABQ79507.
XX	Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g.	
PT	MURF1, MURF3 or MAFBX, useful for treating muscle atrophy and other	
PT	related disorders, e.g. Guillian-Barre syndrome, peripheral neuropathy,	
PT	and nerve damage.	
XX	Claim 1; Fig 9;	104pp; English.
PS	The invention relates to isolated nucleic acid molecules encoding muscle	
XX	atrophy proteins MURF1, MURF3, or MAFBX. The proteins can be expressed by	
CC	standard recombinant methodology. The nucleic acid molecules and	
CC	polypeptides are useful for treating muscle atrophy or detecting atrophy,	
CC	and for treating related diseases/disorders, e.g. Guillian-Barre	
CC	syndrome, peripheral neuropathy, or nerve damage caused by environmental	
CC	toxins or drugs. The MURF1, MURF3 and MAFBX antagonists, and the	
CC	antagonists of their pathways are useful for inhibiting atrophy, inducing	
CC	hyperatrophy, decreasing ubiquitination, interfering with the ubiquitin	
CC	pathway, or modulating MURF1, MURF3 or MAFBX expression or activity. The	
CC	nucleotide sequences are useful for diagnostic and genetic testing. The	
CC	present sequence represents a human MURF1 protein	
XX	Sequence 340 AA;	
SQ		
Alignment Scores:		
Pred. No.:	4,56e-126	Length: 340
Score:	1562.00	Matches: 235
Percent Similarity:	98.08%	Conservative: 12
Best Local Similarity:	94.25%	Mismatches: 6
Query Match:	54.85%	Indels: 0
DB:	5	Gaps: 0
US-10-775-649-5 (1-1597) x ABB81135 (1-340)		
Qy	338	ATGAGAACCTGGAGAACGACGTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCT 337
Db	1	MetGluAsnLeuGluLysGlnLeuileCysProlleCysLeuGluMetPheThrLysPro 20
Qy	398	GTGGTTCATCTCGCCCTGCCAACAACCTCTCGCCGAGTGTCGCACACATCTTCCAG 457

Db 21 ValValilleLeuProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspIlePheGln 40  
QY 458 GCTGCGAATCCCTACTGAGCAACCGGGCTCAGTGTCCATGTCCTGAGGTCTTTC 517  
Db 41 AlaAlaAsnProTyrTrpThrSerArgLysSerValSerMetSerGlyArgPhe 60  
QY 518 CGTTGCCCTCTGTCGCGCCATGATGATCATGCGGCGGCGGCTGTCGCGCTGAG 577  
Db 61 ArgCysProThrCysArgHisGluValIleMetAspArgHisGlyValTyrGlyLeuGln 80  
QY 578 AGAAGCTGCTGTGTGGAACATCATTCATACAGCAGAGTGTCTCAGTCGCGCC 637  
Db 81 ArgAsnLeuValGluAsnIleAspIleTyrLysGlnGluCysSerSerArgPro 100  
QY 638 CTCGAGAAAGGCGCACCGATGTCAGAGACAGACAGAGAGATCAACATCTAC 697  
Db 101 LeuGlnLysGlySerHisProMetCysLysGluHisGluAspGluLysIleAsnIleTyr 120  
QY 698 TGTCTCACGTGTGAGGTGCTTACTTCTCTTGTGCAAGGTGTTTGGGGCTCACAGGCC 757  
Db 121 CysLeuThrCysGluValProThrCysSerMetCysLysValPheGlyIleHisLysAla 140  
QY 758 TGTGAGGTGCGCTTGTGCAAGCATCTTCCAGGACAGAGACTGAGTGAAGTGC 817  
Db 141 CysGluValAlaProLeuGlnSerValPheGlnGlyGlnLysThrGluLeuAsnAsnCys 160  
QY 818 ATCTCCATGCTGTGCGGGAACGACGAGTGCAGACGATCATCTCAGCTGGAGGAC 877  
Db 161 IleSerMetLeuValAlaGlyAsnAspArgValGlnThrIleIleThrGlnLeuGluAsp 180  
QY 878 TCGTGACAGTGCACCAAGGAGATGCCACCGAGGTGAAGGAGGAGCTGAGTCAGAAAGTTT 937  
Db 181 SerArgValThrLysGluAsnSerHisGlnValLysGluLeuSerGlnLysPhe 200  
QY 938 GACACCTCTACCCATCTCTGATGATAGAGAGAGAGAGCTGCTGAGCGGATCAGCAG 997  
Db 201 AspThrLeuTyrAlaIleLeuAspGluLysLysSerGluLeuLeuGlnArgIleThrGln 220  
QY 998 GACGAGGAGAGAGTGGCTTCATCGAGGCTCTGATCTCCAGTACAGGAGGAGCTG 1057  
Db 221 GluGlnGluLysLeuSerPheIleGluAlaLeuIleGlnGlnThrGlnGlnLeu 240  
QY 1058 GAAAGTCCACCAAGCTTGTGAGACCGCCATCCAGTCCCTGATGAGCCCGAGGGCT 1117  
Db 241 AspLysSerThrLysLeuValGluThrAlaIleGlnSerLeuAspGluProGlyGlyAla 260  
QY 1118 ACCTTCTCTCAGTGCAGAGCTCATCAGAGCATTTGAGAGCTTCTCAGGCTGCTC 1177  
Db 261 ThrPheLeuLeuThrAlaLysGlnLeuIleLysSerIleValGluAlaSerLysGlyCys 280  
QY 1178 CAGCTGGGGAAGACAGAGCAAGCTTTGAGAACATGACTTACTTCTGAGCTTAGAA 1237  
Db 281 GlnLeuGlyLysThrGluGlnGlyPheGluAsnMetAspPhePheThrLeuAspLeuGlu 300  
QY 1238 CACATGACAGAGCTTGTGAGGCGCATGACTTTGGGACA 1276  
Db 301 HisIleAlaAspAlaLeuArgAlaIleAspPheGlyThr 313

RESULT 13

AA000998

ID AA000998 standard; protein; 302 AA.

XX

AC AA000998;

XX

DT 01-OCT-2001 (first entry)

XX

DE Human bone marrow protein, SEQ ID NO: 499.

XX

KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;

KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;

KW immunosuppressive; gene therapy; cytokine cell proliferation;

KW cell differentiation modulator; immune disorder; infection; cancer;

KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

XX Homo sapiens.  
OS WO200153453-A2.  
PN 26-JUL-2001.  
XX 23-DEC-2000; 2000WO-US034960.  
XX 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00682191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 30-NOV-2000; 2000US-0250583P.  
XX (HYSE-) HYSEQ INC.  
XX Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;  
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Drmanac RT;  
XX WPI; 2001-488707/53.  
DR N-PSDB; AAH90117.  
XX Novel bone-marrow-expressed polynucleotides and polypeptides, useful for  
PT treating e.g. cancer and immune deficiency disorders.  
XX Claim 10; Page 646; 648pp; English.  
XX The present sequence is one of 251 novel human polypeptides encoded by a  
CC bone marrow-expressed polynucleotide. The polynucleotide and the  
CC polypeptide encoded by it are useful in the treatment of various immune  
CC deficiencies and disorders. The deficiencies and disorders may be  
CC genetic, may be caused by a viral (e.g. HIV), bacterial or fungal  
CC infection, or may result from an autoimmune disorder, a coagulation  
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,  
CC suppression of an inflammatory response or treatment of a nervous system  
CC disorder such as Alzheimer's disease. Detection of the presence or  
CC increased expression of the polynucleotide or the protein it encodes is  
CC useful for the diagnosis and/or prognosis of one or more types of cancer.  
CC The polynucleotide and polypeptide can be used as nutritional sources or  
CC supplements and in the screening of chemical compounds as potential drugs  
XX

SQ Sequence 302 AA;

Alignment Scores:  
Pred. No.: 3,76e-110 Length: 302  
Score: 1378.00 Matches: 259  
Percent Similarity: 97.46% Conservative: 10  
Best Local Similarity: 93.84% Mismatches: 7  
Query Match: 48.38% Indels: 0  
DB: 4 Gaps: 0

US-10-775-649-5 (1-1597) x AA000998 (1-302)

QY 299 ATGGATTATAATCTAGCCTGATTCCTGATGAAACGCTATGGAGAACCTGGAGAGCAG 358  
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20  
QY 359 CTGATCTGCCCATCTGCTCGGAGATGTTTACCAAGCCTGTGTCTATCTCGCCCTCCAA 418  
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
QY 419 CACAACCTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGACC 478  
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTTPThr 60  
QY 479 AACCGGCTGGCTGAGTGTCCATGTCTGAGGTGCTTCCGTTCCGCTGCGCCCTCCCAT 538  
:::|||||



Db 111 Glu---SerThrArgProGluLysLysSerAspGlnProMetCysGluGluHisGluGlu 129  
QY 680 GAGAGATCAACATCTACTCTCTCACGTGTGAGGTGCTACTCTGCTCCCTGTGTCAGAGTG 739  
Db 130 GluArgIleAsnIleTyrCysLeuAsnCysGluValProThrCysSerLeuCysLysVal 149  
QY 740 TTTGGGGCTCACGAGCCTGTGAGGTGGCCCTTTCGAAAGCATCTTCCAAAGGACAGAAG 799  
Db 150 PheGlyAlaHisLysAspCysGlnValAlaProLeuThrHisValPheGlnArgGlnLys 169  
QY 800 ACTGACTGAGTAACCTGATCTCCATCTGCTGTGGCGGGGACACGAGTGCGAGCATC 859  
Db 170 SerGluLeuSerAspGlyIleAlaIleLeuValGlySerAsnAspArgValGlnGlyVal 189  
QY 860 ATCTCTCAGCTGAGGACTGCTCAGAGTCACCAAGAGGAAATAGCACACGAGTGAAGGAG 919  
Db 190 IleSerGlnLeuGluAspThrCysLysThrIleGluGluCysCysArgLysGlnLysGln 209  
QY 920 GAGCTGAGTCAGAAGTTTGACACCCCTCTAGCCATCTGATGAGAAGAGCGAGCTG 979  
Db 210 GluLeuCysGluLysPheAspTyrLeuTyrGlyIleGluGluArgLysAsnGluMet 229  
QY 980 CTCACGGGATCAGCAGGAGGAGGAGAGCTGGCTTCATCCAGGCTCTGATCCTC 1039  
Db 230 ThrGlnValIleThrArgThrGlnGluGluLysLeuGluHisValArgAlaLeuIleLys 249  
QY 1040 CAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTGTGGAGACCGCCATCCAGTCCCTG 1099  
Db 250 LysTyrSerAspHisLeuGluAsnValSerLysLeuValGluSerGlyIleGlnPheMet 269  
QY 1100 GATGAGCCCGAGGGCTACCTTCTCTCAAGTGCCCAAGCAGCTCATCAAGAGCATGTGA 1159  
Db 270 AspGluProGluMetAlaValPheLeuGlnAsnAlaLysThrLeuLysLysIleSer 289  
QY 1160 GAAGCTCCAGGCTGCCAGCTGGGGAAGACAGACCAAGCGCTTTCAGAACATGAGCTAC 1219  
Db 290 GluAlaSerLysAlaPheGlnMetGluLysIleGluHisGlyTyrGluAsnMetAsnHis 309  
QY 1220 TTTACTCTGACTTAGAACATAGCAGAGGCGCTTGAGGGCCATTCACCTT 1270  
Db 310 PheThrValAsnLeuAsnArgGluGluLysIleIleArgGluIleAspPhe 326

RESULT 15  
ADB64249  
ID ADB64249 standard; protein; 452 AA.  
XX  
AC ADB64249;  
XX  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human protein encoded by clone DFNS20073320.  
XX  
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
KW cell regeneration; membrane protein; signal transduction-related protein;  
KW transcription-related protein; osteoporosis; neurological disease;  
KW cancer; tumour.  
XX  
XX Homo sapiens.  
XX  
PN EP1308459-A2.  
XX  
PD 07-MAY-2003.  
XX  
XX 28-MAR-2002; 2002EP-00007401.  
XX  
XX 05-NOV-2001; 2001JP-00379298.  
PR 25-JAN-2002; 2002US-00350978.  
XX  
XX (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX  
DR WPI: 2003-450961/43.  
DR N-PSDB; ADB62279.  
XX  
PT New polynucleotides and polypeptides, useful for developing a diagnostic  
PT marker or medicines for regulation of their expression and activity, or  
PT as targets of gene therapy.  
XX  
PS Claim 1; Page; 222pp; English.  
XX  
CC The invention discloses a polynucleotide comprising a sequence selected  
CC from 1970 fully defined nucleotide sequences which encode novel  
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
CC or its partial peptide, an antibody binding to the polypeptide or peptide  
CC of the polynucleotide, immunologically assaying the polypeptide or  
CC peptide of the polynucleotide by contacting the polypeptide or peptide  
CC with the antibody of the encoded protein, and observing the binding  
CC between the two, a transformant carrying the polynucleotide in an  
CC expressible manner and an antisense polynucleotide. The oligonucleotide  
CC is useful as a primer for synthesising the polynucleotide, or as a probe  
CC for detecting the polynucleotide. The polynucleotides and encoded  
CC proteins are useful as pharmaceutical agents and many disease-related  
CC genes may be included in them, for developing a diagnostic marker or  
CC medicines for regulation of their expression and activity, or as targets  
CC of gene therapy. The genes are involved in tissue and/or cell  
CC regeneration. Membrane proteins, signal transduction-related proteins,  
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate  
CC the activity or expression of the encoded protein to treat diseases. The  
CC sequence presented is a protein of the invention. Note: Some of the  
CC sequence data for this patent is not represented in the printed  
CC specification, but is based on sequence information supplied by the  
CC European Patent Office.  
XX  
SQ Sequence 452 AA;

Alignment Scores:  
Pred. No.: 2,79e-88 Length: 452  
Score: 1126.50 Matches: 221  
Percent Similarity: 67.00% Conservative: 45  
Best Local Similarity: 55.67% Mismatches: 60  
Query Match: 39.55% Indels: 71  
DB: 7 Gaps: 2  
US-10-775-649-5 (1-1597) x ADB64249 (1-452)

QY 80 ATGAGCATTCTCTGAATTACAAGTCTTTCTCCAAGAGCAGCAGCATGGATACTTG 139  
Db 1 MetSerAlaSerLeuAsnTyrLysSerPheSerLysGluGlnThrMetAsp----- 18  
QY 140 GAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCCAGAGCCTGTGTCATCTC 199  
Db 18 ----- 18  
QY 200 CCTTGCACGACACCTGTGTGAGGAAATGTGCGGGCCCCCTTGGAGACAAAGACTTGT 259  
Db 18 ----- 18  
QY 260 GTGACGCGAGTGGGCAAGACAGTCGCATTTCAAAGCAATATGATTTAAATCTAGCCTG 319  
Db 18 ----- 18  
QY 320 ATTCTGATGGAAACGCTATGGAGAACCTGGAGAGCAGCTGATCTGCCCCATCTCCCTG 379  
Db 19 -----AsnLeuGluLysGlnLeuLeuCysProIleCysLeu 30  
QY 380 GAGATGTTTACCAAGCCTGTGGTCTCTCTGCTTCCCAACACAACTCTGCCGGAAGTGT 439  
Db 31 GluMetPheThrLysProValValIleLeuProCysGlnHisAsnLeuLysCysArgLysCys 50  
QY 440 GCCAACGACATCTTCCAGGCTCGGAATCCCTACTGTGACCAACCGCGGTGGCTCAGTGTCC 499



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QY 458 GCTGCGAATCCCTACTGACCAACCGCGGTGGCTCAGTGTCCATGTCAGGTGCTTTC 517
Db 39 ---ValSerHisCysAlaThrAsnGlu-----SerValGlu---SerIleThrAlaPhe 54
QY 518 CGTTGCCCTCTGTCGCCCATGAGTATGATCATGACCGCGGACGCGGTGTACGCGCTGCAG 577
Db 55 GlnCysProThrCysArgHisValIleThrLeuSerGlnArgGlyLeuAspGlyLeuLys 74
QY 578 AGGAACCTGCTGGTGAACATCATTCATGACATCTACAAG----- 616
Db 75 ArgAsnValThrLeuGlnAsnIleIleAspArgPheGlnLysAlaSerValSerGlyPro 94
QY 616 ----- 616
Db 95 AsnSerProSerGluThrArgArgGluArgAlaPheAspAlaAsnThrMetThrSerAla 114
QY 617 -----CAGGAGTGTCTCCAGTGCGCCCTGCAG----- 643
Db 115 GluLysValLeuCysGlnPheCysAspGlnAspProAlaGlnAspAlaValLysThrCys 134
QY 644 -----AAAGGCAGCCACCG----- 658
Db 135 ValThrCysGluValSerTyrCysAspGluCysLeuLysAlaThrHisProAsnLysLys 154
QY 659 -----ATG 661
Db 155 ProPheThrGlyHisArgLeuIleGluProIleProAspSerHisIleArgGlyLeuThr 174
QY 662 TCAAGGACACGAGACGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCCTACT 721
Db 175 CysLeuGluHisGluAspGluLysValAsnMetTyrCysValThrAspAspGlnLeuIle 194
QY 722 TGCTCTTTGCAAGTGTGGGCTCACCAGGCTGTGAGTGTCCCTTTGCAAGC 781
Db 195 CysAlaLeuCysLysLeuValGlyArgHisArgAspHisGlnValAlaAlaLeuSerGlu 214
QY 782 ATCTTCCAAGGACAGAGAGTGTGAGTGTGAGTGTCTCAGTGTGAGGTGCCTACT 841
Db 215 ArgTyrAspLysLeuLysGlnAsnLeuGluSerAsnLeuThrAsnLeuLysArgAsn 234
QY 842 GACCGAGTGCAGCATCTCTCAGTGGAGGACTCGTGCAGAGTGCACCAAGGAGAT 901
Db 235 ThrGluLeuGluThrLeuAlaLysLeuIleGlnThrCysGlnHisValGluValAsn 254
QY 902 AGCCACCGGTGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 961
Db 255 AlaSerArgGlnGluAlaLysLeuThrGluGluCysAspLeuLeuIleGlnIleGln 274
QY 962 GAGAAGAGGAGGAGTGTGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1021
Db 275 GlnArgArgGlnIleIleGlyThrLysIleLysGluGlyValMetArgLeuArgLys 294
QY 1022 ATCGAGGCTGTGATCTCCAGTACAGGAGGAGTGTGAAAGTCCACCAAGCTTGGAG 1081
Db 295 LeuAlaGlnIleAlaAsnCysLysGlnCysIleGluArgSerAlaSerLeuIleSer 314
QY 1082 ACCGCATCCAGTCTCCGATGAGCGCGGAGGAGTGTCTCTCAAGTGTCCAGCAG 1141
Db 315 GlnAlaGluHisSerLeuLysGluAsnAspHisAlaArgPheLeuGlnThrAlaLysAsn 334
QY 1142 CTCATCAAGAGCATTTAGAACCTCAAGGCTGCGAGTGTGGGAGACAGACGAGCAG 1201
Db 335 IleThrGluArgValSerMetAlaThrAlaSerSerGlnValLeuIleProGluIleAsn 354
QY 1202 TTT---GAGAACATGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCCTTGAGG 1258
Db 355 LeuAsnAspThrPheAspThrPheAlaLeuAspPheSerArgGluLysLysLeuLeuGlu 374
QY 1259 GCCATTGACTTTGGGACA 1276
Db 375 CysLeuAspTyrLeuThr 380
```

## RESULT 2

```
T09013
RING finger protein Fxy - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
C/Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A>Title: A gene spans the pseudoautosomal boundary in mice.
A/Reference number: Z16531; MUID:98004518; PMID:9342357
A/Accession: T09013
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-667 <PAL>
A/Cross-references: EMBL:AF026565; NID:g2589222; PIDN:AAB83986.1; PID:g2589223
C/Genetics:
A:Gene: Fxy
A:Map position: X; Y
C:Superfamily: rfp transforming protein
C:Keywords: zinc finger
P:6-65/Domain: RING finger homology <RRN>

Alignment Scores:
Pred. No.: 3,73e-23 Length: 667
Score: 426.50 Matches: 105
Percent Similarity: 46.11% Conservative: 73
Best Local Similarity: 27.20% Mismatches: 129
Query Match: 14.98% Indels: 79
DB: 2 Gaps: 7

US-10-775-649-5 (1-1597) x T09013 (1-667)
QY 338 ATGGAGAACCTGAGAGACGAGCTGATCTGCCCATCTGCTGAGATGTTTACCAGCCT 397
Db 1 MetGluThrLeuGluSerGlnLeuThrCysProIleCysLeuGluLeuPheGluAspPro 20
QY 398 GTGGTGCATCTCTCCCTGCCCAACACCACTCTGCCGAGTGTGCCAACACACATCTTCCAG 457
Db 21 ---LeuLeuLeuProCysAlaHisSerLeuCysPheAsnCysAlaHisArgIleLeu--- 38
QY 458 GCTGCGAATCCCTACTTGGACCAACCGCGGTGCTCAGTGTCCATGTCGTGAGGTGCTTTC 517
Db 39 ---ValSerHisCysAlaThrAsnGluProValGlu-----SerIleAsnAlaPhe 54
QY 518 CTTTCCCTCTGTCGCCCATGAGTATGATCATGAGCGGACGCGGAGTGTACGCGCTGCAG 577
Db 55 GlnCysProThrCysArgHisValIleThrLeuSerGlnArgGlyLeuAspGlyLeuLys 74
QY 578 AGGAACCTGCTGGTGAACATCATTCATGACATCTACAAG----- 616
Db 75 ArgAsnValThrLeuGlnAsnIleIleAspArgPheGlnLysAlaSerValSerGlyPro 94
QY 616 ----- 616
Db 95 AsnSerProSerGluThrArgArgGluArgAlaPheAspAlaAsnThrMetSerSerAla 114
QY 617 -----CAGGAGTGTCTCCAGTGCGCCCTGCAG----- 643
Db 115 GluLysValLeuCysGlnPheCysAspGlnAspProAlaGlnAspAlaValLysThrCys 134
QY 644 -----AAAGGCAGCCACCG----- 658
Db 135 ValThrCysGluValSerTyrCysAspGluCysLeuLysAlaThrHisProAsnLysLys 154
QY 659 -----ATG 661
Db 155 ProPheThrGlyHisArgLeuIleGluProIleProAspSerHisIleArgGlyLeuThr 174
QY 662 TCAAGGACACGAGACGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCCTACT 721
Db 175 CysLeuGluHisGluAspGluLysValAsnMetTyrCysValThrAspAspGlnLeuIle 194
QY 722 TGCTCTTTGCAAGTGTGGGCTCACCAGGCTGTGAGTGTCCCTTTGCAAGC 781
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[illegible]

76	GGAAATGAGCACTTCTCTGAAATTAACAAGTCTTTCTTCCAAAGACGACGACGACCATGATGATAA	135
65	GlnAsnGluTrpValAspLysSerArgLeuValLeuThrLysProProLysGluGlyGlu	84
136	CTTGGA-----AAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCAAGAA	183
85	ThrAsnGlyThrAspGlnGluValThrAspThrAlaGluGlnPro-----	99
184	GCCTGTGGTCATTCTCCCTTGCCA--GCACAACTGTGTCAGGAAATATGTGCGGGCCCCCCC	240
100	-----AspSerLysThrProGlnLysArgLysLeuLeuGluGluProGluProGluPro	116
241	TTGAGACAAAGACTTGGTGTGACGCGAGTGGCGAAGACAGTGCATTTTCAAGACCAATAT	300
117	LysLeuAlaLysVal-----GluGluLysAspAlaSerLys--Asn--	129
301	GGATTATAAATCTAGCCTCATCTCTGATGMAACGCTATGGAGAACTCGAGAGAGCAGCT	360
130	-----AlaSerSerLeu-----GlyAlaAlaGlyAspPheAlaGluGluLe	143
361	GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGGTTCATCTGCTCCCTGCCCAACA	420
143	uThrCysProLeuCysValGluLeuPheLysAspProValMetVal--AlaCysGlyHi	162
421	CAACTCTCCGGAAGTGTGCCAACACATCTTCCAGGCTGCGAATCCCTACTTGGACCAA	480
162	sAsnPheCysArgSerCysIleAspLysAlaTrpGluGlyGlnSer-----	177
481	CGCGGTGCTCAGTGTCTCATCTGTGGAGTGTGTTTCGTTGGCTTCGCTGCGCCCATGA	540
178	-----SerPheAlaCysProGluCysArg--G	186
541	AGTGATCATGGACCGGCACGGGTGTACGGCTGCAGAGGAACCTGTGTTGTGAAACAT	600
186	uSerIleThrAspArgLys-----TyrThrIleAsnArg-----ValLeuAlaLeuLe	202
601	CATTGACATCTCAAGCAGGAGTGTCCAGT---CGGCCCCCTGCAGAAAGCGCACCC	657
202	uAlaLys-----LysAlaAlaCysThrProValThrProValGluLysLysThrArgPr	220
658	GATG-----TGCAGGAACACGAAACAGAGAAGATCAACATCTACTGTCTCAGTGTGA	711
220	oLeuGluLysCysSerGluHis---AspGluArgLeuLysLeuTyrCysLysAspAspG	239
712	GGTGCCTACTTGTCTCTGTGCAAGTGTGTTGGGGCTCACACGGCTGTGAGGTGCCCC	771
239	yThrLeuSerCysValIleCysArgAspSerLeuLysHisAlaSerHisAsnPheLeuPr	259
772	TTTGCAAGCATCTTCCAAAGCAGAGCACTGTGAGTGTGAGTAACCTGCATCTCCATGCTGGT	831
259	oIleLeuAspAlaValGlyValTyrArgGluGluLeuSerAlaIleValAlaProLeuG	279
832	GGCGGGGAACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTGCAGAGTCAC	891
279	uAlaSerLeuLysValThrGluGlnLeuSerSerGluGlnSerAspLysIleGluGlnHi	299
892	CAAGGAATAGCCACAGTGTGAAGCGAGGAGCTGAGTCAAGCTTTTGACACCTCTTACGC	951
299	sAsnLysAsnMetSerGlnTyrLysGluHisIleThrSerGluPheGluLysLeuHisLy	319
952	CATCTCTGGATGAGAAAGACGACGCTGTGTGACGCGATCACACGAGGACGAGGAGAGAA	1011
319	sPheLeuArgGluArgGluGluLysLeuLeuGluGlnLeuLysGluGlnGlyGluAsnLe	339
1012	GCTTGGCTTCATCGAGGCTCTGATCTCTCCAGTACAGGGGACGAGCTGTGAAAGTCCACAA	1071
339	uLeuThrGluMetGluAsnAsnLeuValLysMetGlnGluSerGlnAspAlaIleLysLy	359
1072	GCTTGTGGACCGCCATCCAGTCCCTTGGATGAGCCGGGGGCTTCTCTCTCTCAAG	1131
359	sThrIleSerLeuAlaLysGluArgMetGluAspThrAspSerIleSerPheMetAs	379





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 15, 2005, 12:34:11 ; Search time 163 Seconds  
(without alignments)  
10034.239 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 2848

Sequence: 1 ctcgagattacccttag.....gaaataaattatctctgtgcc 1597

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p,model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool.p/US10775649/runat.14062005.141110.20658/app\_query.fasta.1.1735  
-DB=UniProt\_03 -QFWI=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL  
-OUTFWT=pt0 -NORM=ext -HRAPSIZB=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10775649 @CGN 1.1 159 @runat.14062005.141110.20658 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=1120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1671	58.7	351	Q91Z63	Q91Z63 rattus norv
2	1613	56.6	346	Q6NR77	Q6NR77 homo sapien
3	1613	56.6	353	1 RN28 HUMAN	Q6NR77 homo sapien
4	1188.5	41.7	356	2 Q6DE39	Q6DE39 xenopus lae
5	1126.5	39.6	540	2 Q81UD9	Q81UD9 homo sapien
6	1120.5	39.3	360	2 Q6INV6	Q6INV6 xenopus lae
7	1119.5	39.3	452	2 Q6EDV3	Q6EDV3 homo sapien
8	1119.5	39.3	548	2 Q6EDV2	Q6EDV2 homo sapien
9	1110	39.0	366	2 Q6ERP3	Q6ERP3 mus musculu
10	1093.5	38.4	436	1 RN29 HUMAN	Q6BYV6 homo sapien
11	1093.5	38.4	532	2 Q6BYV5	Q6BYV5 homo sapien
12	1092.5	38.4	342	2 Q6BYV3	Q6BYV3 homo sapien
13	1062.5	37.3	384	2 Q6BYV2	Q6BYV2 homo sapien
14	1036.5	36.4	443	2 Q6DHS0	Q6DHS0 brachydanio
15	933	32.8	345	2 Q6IQH8	Q6IQH8 brachydanio
16	914.5	32.1	348	2 Q7ZWH0	Q7ZWH0 brachydanio

17	862.5	30.3	225	2	Q9GMX4	Q9GMX4 macaca fasc
18	831.5	29.2	241	2	Q8IU54	Q8IU54 homo sapien
19	820.5	28.8	197	2	Q8C6Y1	Q8C6Y1 mus musculu
20	807	28.3	429	2	Q6DC78	Q6DC78 brachydanio
21	611.5	21.5	151	2	Q8BWC4	Q8BWC4 mus musculu
22	457.5	16.1	498	2	Q6NT41	Q6NT41 homo sapien
23	455	16.0	524	2	Q6ZRL7	Q6ZRL7 homo sapien
24	453.5	15.9	498	2	Q6NT17	Q6NT17 homo sapien
25	448.5	15.7	498	2	Q9BGS5	Q9BGS5 macaca fasc
26	447	15.7	551	2	Q9H5P2	Q9H5P2 homo sapien
27	447	15.7	759	2	Q7Z4K8	Q7Z4K8 homo sapien
28	442	15.5	644	2	Q95J41	Q95J41 macaca fasc
29	441	15.5	441	2	Q64LM2	Q64LM2 mus musculu
30	441	15.5	759	2	Q7TNM2	Q7TNM2 mus musculu
31	435	15.3	693	2	Q6PH04	Q6PH04 brachydanio
32	434.5	15.3	667	1	MID1 RAT	P82458 rattus norv
33	433.5	15.2	667	2	Q71R46	Q71R46 gallus gall
34	433	15.2	424	2	Q6P119	Q6P119 mus musculu
35	432.5	15.2	667	1	MID1 HUMAN	Q15344 homo sapien
36	432.5	15.2	667	2	Q90WD1	Q90WD1 gallus gall
37	432.5	15.2	680	1	MID1 MOUSE	Q05833 mus musculu
38	432	15.2	668	2	Q6DEU6	Q6DEU6 xenopus tro
39	426	15.0	729	2	Q7TNM1	Q7TNM1 mus musculu
40	425	14.9	728	2	Q9NQ86	Q9NQ86 homo sapien
41	424.5	14.9	667	1	MID1 MUSSP	P82457 mus spretus
42	418	14.7	733	2	Q6NU77	Q6NU77 xenopus lae
43	407	14.3	729	2	Q80WG7	Q80WG7 mus musculu
44	402.5	14.1	685	1	MID2 MOUSE	Q9QU56 mus musculu
45	402.5	14.1	685	2	Q6GX19	Q6GX19 aotus trivi

#### ALIGNMENTS

RESULT 1  
Q91Z63 PRELIMINARY; PRT; 351 AA.  
ID Q91Z63  
AC Q91Z63;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Muscle ring finger protein 1 (Ring finger protein 28).  
GN Name=Rnf28;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=21578247; PubMed=11679633; DOI=10.1126/science.1065874;  
RA Bodine S.C., Latres E., Baumhueter S., Lai V.K.-M., Nunez L.,  
RA Clarke B.A., Poueymirou W.T., Panaro F.J., Na B., Dharmarajan K.,  
RA Pan Z.-Q., Valenzuela D.M., DeChiara T.M., Stitt T.N.,  
RA Yancopoulos G.D., Glass D.J.;  
RT "Identification of ubiquitin ligases required for skeletal muscle atrophy.";  
RL Science 294:1704-1708(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Krzyzanski M.I., Skalka U., Smilun D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
DR EMBL; AY059627; AL16405.1; -;  
DR EMBL; BC061824; AH61824.1; -;  
DR HSSP; P38399; 1JM7.  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR Pfam; PF00643; zf-B\_box; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR PROSITE; PS00119; ZF\_BBOX; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; 1.  
DR PROSITE; PS00089; ZF\_RING\_2; 1.  
KW Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 351 AA; 39723 MW; BF906A21340C4D97 CRC64;

Alignment Scores:  
Pred. No.: 2,03e-106 Length: 351  
Score: 1671.00 Matches: 319  
Percent Similarity: 98.16% Conservative: 1  
Best Local Similarity: 97.85% Mismatches: 6  
Query Match: 58.67% Indels: 0  
DB: 2 Gaps: 0

US-10-775-649-5 (1-1597) x Q91Z63 (1-351)

QY 299 ATGGATTATTAATCTAGCTGATCTCTGATGGAACCTATGAGAACCTGGAGAGCAG 358  
DB 1 MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20  
QY 359 CTGATCTGCCCATCTGCTGGAGAGTTTACCAAGCCTGTGTATCTGCTGCCCTCCAA 418  
DB 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40  
QY 419 CACAACCTCTGCCGGAAGTGTGCCAACGACATCTCCAGGCTGCGAATCCCTACTGGACC 478  
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60  
QY 479 AACCGGCTGGCTCAGTGTCCATGTCTGGAGTGTCTTCCGTTGCCCTCGTCCGCCCAT 538  
DB 61 AsnArgGlyLysSerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80  
QY 539 GAAGTATCATGACCGCAGCGGGGTGACGGCTGCAGAGAACCTGCTGGTGGGAAAC 598  
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100  
QY 599 ATCATTGATCATACAGCAGGAGTCTCCAGTCCGCCCCCTCGAGAAAGCAGCCACCG 658  
DB 101 IleIleAspIleTyrLysGlnCysSerArgProLeuGlnLysGlySerHisPro 120  
QY 659 ATGTGCAAGNACACGACGAGATCATCTACTGTCTACGTGTGAGTGGCT 718  
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
QY 719 ACTTGCTCTCTGCAAGTGTGTTGGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAA 778  
DB 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
QY 779 AGCATCTTCCAGGACAGAACTGAGTGAATCTGATCTCCATGTCTGTGGCGGG 838

DB 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGCAGACGATCATCTCTAGCTGGAGGACTCTGCGAGAGTACCAGGAG 898  
DB 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
QY 899 AATAGCCACAGCTGAAGGAGGAGCTGAGTCAAGAGTTTGCACACCTCTACGCCATCTG 958  
DB 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220  
QY 959 GATGAGAAGACGAGCTGCTGCAGCGGATCACGACGAGCAGGAGAGAGCTGGGC 1018  
DB 221 AspGluLysLysSerGluLeuGlnArgIleThrGlnGlnGlnGlnGluLysLeuAsp 240  
QY 1019 TTCATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGG 1078  
DB 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260  
QY 1079 GAGACCGCATCCAGTCCCTGGATGAGCCGAGGGGCTTACCTTCTCTCAAGTGCAG 1138  
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280  
QY 1139 CAGCTCATCAAGCAGCATTGTAGAAGCTCCAAAGGCTGCCAGCTGGGGAGACAGACAA 1198  
DB 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
QY 1199 GCCTTGTGAACATGAGTACTTCTTCTGAGCTTAGACACATAGCAGAGCCTTGAGG 1258  
DB 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320  
QY 1259 GCCATTGACTTTGGGACA 1276  
DB 321 AlaIleAspPheGlyThr 326

RESULT 2  
Q6NR77 PRELIMINARY; PRT; 346 AA.

AC Q6NR77; TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Ring finger protein 28.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Bisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
DR EMBL; BF007373; AAP36037.1; -;  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro; IPR004931; Pro/parathymosin.  
DR InterPro; IPR000315; Znf Bbox.  
DR InterPro; IPR001841; Znf ring.  
DR Pfam; PF03247; Prothymosin; 1.  
DR Pfam; PF00643; zf-B\_box; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00336; BBOX; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS00119; ZF\_BBOX; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; 1.  
DR PROSITE; PS00089; ZF\_RING\_2; 1.  
KW Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 346 AA; 39275 MW; F835CA80F7CF53FA CRC64;

Alignment Scores:

Pred. No.:	1.97e-102	Length:	346
Score:	1613.00	Matches:	305
Percent Similarity:	96.95%	Conservative:	13
Best Local Similarity:	92.99%	Mismatches:	10
Query Match:	56.64%	Indels:	0
DB:	2	Gaps:	0
US-10-775-649-5 (1-1597) x QGNR77 (1-346)			
QY	299	ATGGATTAAATCTAGCTGATTCCTGATGAAACGCTATGAGAACCTGGAGAGCAG	358
DB	1	MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln	20
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGGTTCATCTGCTGCCGCA	418
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40
QY	419	CACACCTCTGCGAAGTGTCCACACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60
QY	479	AACCCGGTGGCTCAGTGCCATGCTCTGGAGTCCGTTTCCGTTGCCCTCGCGCCCAT	538
DB	61	SerArgGlySerSerValSerMetSerGlyArgPheArgCysProThrCysArgHis	80
QY	539	GAAGTGATCATGCGCGCAGCGGTGTACGCCCTGCAGAGGAACCTGCTGGTGGAAAC	598
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100
QY	599	ATCATGTGATCATACAGCAGAGTGTCTCCAGTCCGCGCCCTGCAGAAAGGACCCG	658
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
QY	659	ATGTGCAAGAACACGAGCAGAGTCAACATCTACTGTCTCACGTGTGAGTGCTCT	718
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140
QY	719	ACTTGCTCTCTGCAAGTGTGTGGGCTCACAGGCTGTGAGGTGTGCCCTTTGCAA	778
DB	141	ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln	160
QY	779	AGCATCTTCCAGGACAGAGTGTGAGTGAATCTGATCTCCATCTGCTGTGGCGGG	838
DB	161	SerValPheGlnGlyLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly	180
QY	839	AACGACGAGTCCAGCATCATCTCTCAGCTGGAGGACTCTGCGAGAGTGCACCAAGAG	898
DB	181	AsnAspArgValGlnThrIleThrGlnLeuGluAspSerArgValThrLysGlu	200
QY	899	AATAGCCACCGGTGAAGGAGGAGTGTGAGTCAAGAGTTTGACACCTCTACGCCATCCTG	958
DB	201	AsnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220
QY	959	GATGAGAACAGAGGAGTGTGCGAGCGGATCATCGCAGGACGAGAGAGCTGGCG	1018
DB	221	AspGluLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuSer	240
QY	1019	TTTCATCGGCTCTGATCTCTCAGTACAGGAGGAGCTGGAAGTCCACCAAGCTTGTG	1078
DB	241	PheIleGluAlaLeuIleGlnGlnThrGlnGluGlnLeuAspLysSerThrLysLeuVal	260
QY	1079	GAGACCGCCATCCAGTCCCTGATGAGCGCGGAGGGGCTACCTTCTCTCAAGTCCCAAG	1138
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys	280
QY	1139	CAGCTCATCAAGCATTTGTAGAGCTCCAGGCTGCAGCTGCGGAGGAGCAGAGCAA	1198
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300
QY	1199	GCCTTTGAAACATGACTTACTCTGGAAGTCTAGACATACAGAGCGCTTGGAG	1258
DB	301	GlyPheGluAsnMetAspPheThrThrLeuAspLeuGluHisIleAlaAspAlaLeuArg	320

QY	1259	GCCATTGACTTTGGACAGGTAAA	1282
DB	321	AlaIleAspPheGlyAlaAlaGlu	328
RESULT 3			
RN28_HUMAN	STANDARD;	PRT;	353 AA.
ID	Q96BQ1; Q96BQ3; Q96BD9; Q9BYV4;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	RING finger protein 28 (Muscle specific ring finger protein 1) (MURF1)		
DE	(Striated muscle RING zinc finger protein) (Iris ring finger protein).		
GN	Name=RN28; Synonyms=IRP, MURF1, SMR2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RX	MEDLINE=21140140; PubMed=11243782; DOI=10.1006/jmbi.2000.4448;		
RA	Centner T., Yano J., Kimura E., McElhinny A.S., Pelin K., Witt C.C.,		
RA	Bang M.-L., Trombitas K., Granzier H., Gregorio C.C., Sorimachi H.,		
RA	Labat S.;		
RT	"Identification of muscle specific ring finger proteins as potential		
RT	regulators of the titin kinase domain."		
RL	J. Mol. Biol. 306:717-726(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21316434; PubMed=11283016; DOI=10.1074/jbc.M011208200;		
RA	Dai K.-S., Liew C.-C.;		
RT	"A novel human striated muscle RING zinc finger protein, SMR2,		
RT	interacts with SMT3b via its RING domain."		
RL	J. Biol. Chem. 276:23992-23999(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Iris;		
RA	Wistow G.;		
RT	"IRF: a novel ring finger protein from iris."		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Skeletal muscle;		
RA	Stanchi F.;		
RT	"Characterisation of MURF2, a new muscle-specific RING finger protein		
RT	of the RBCC family that associates with microtubules."		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Skeletal muscle;		
RX	PubMed=14702039; DOI=10.1038/ng1285;		
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,		
RA	Kamatsa A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,		
RA	Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,		
RA	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,		
RA	Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,		
RA	Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H.,		
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,		
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,		
RA	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,		
RA	Fujimori K., Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y.,		
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,		
RA	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,		
RA	Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,		
RA	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,		
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,		
RA	Moriya S., Momiyama H., Satoh N., Takami S., Shimizu Y., Suzuki O.,		
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Terashima Y., Wakebe H.,		
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,		
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,		
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,		
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,		
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45 (2004).  
RN [6].  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP TISSUE=Skin;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- SUBUNIT: Interacts with SM3b and titin.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q969Q1-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q969Q1-2; Sequence=VSP\_005756;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Muscle specific.  
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a  
CC frameshift in position 142.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AJ291713; CAC33173.1; -;  
CC EMBL: AF361946; AAK52497.1; ALT\_FRAME.  
CC EMBL: AF353673; AAK39519.1; -;  
CC EMBL: AJ276484; CAC81706.1; -;  
CC EMBL: AK056942; BAB71318.1; -;  
CC EMBL: BC015717; AAH15717.1; -;  
CC HSSP: P38398; 1JM7.  
CC Genew: HGNC:16007; RNF28.  
CC H-InvDB: HIX0000284; -;  
CC MIM: 606131; -;  
CC GO: GO:0005737; C:cytoplasm; NAS.  
CC GO: GO:0005874; C:microtubule; NAS.  
CC GO: GO:0004871; F:signal transducer activity; NAS.  
CC GO: GO:0007165; P:signal transduction; NAS.  
CC InterPro: IPR008938; ARM.  
CC InterPro: IPR000315; Znf\_Box.  
CC InterPro: IPR001841; Znf\_ring.

DR Pfam: PF00643; zf-B\_box; 1.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00336; BBOX; 1.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS0119; ZF\_BOX; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; 1.  
DR PROSITE: PS00089; ZF\_RING\_2; 1.  
KW Alternative splicing; Coiled coil; Nuclear protein; Zinc-finger.  
FT ZN\_FING 23 79 RING-type.  
FT ZN\_FING 117 159 B\_box-type.  
FT DOMAIN 207 269 Coiled coil (Potential).  
FT VARSPPLIC 1 13 Missing (in isoform 2).  
FT FTID=VSP\_005756.  
FT CONFLICT 237 237 K -> E (in Ref. 1 and 6).  
FT CONFLICT 326 353 TDEEEEFEEEDQEEESTEGKEGHQ -> AAEDDEDDDD  
FT VTIKKQKTDEDD (in Ref. 6).  
SQ SEQUENCE 353 AA; 40247 MW; 9B4B1505039BC86 CRC64;  
Alignment Scores:  
Pred. No.: 1-98e-102 Length: 353  
Score: 1613.00 Matches: 305  
Percent Similarity: 97.55% Conservatives: 13  
Best Local Similarity: 93.56% Mismatches: 8  
Query Match: 56.64% Indels: 0  
DB: 1 Gaps: 0  
US-10-775-649-5 (1-1597) x RN28\_HUMAN (1-353)  
QY 299 ATGGATTATTAATCTAGCTGATTCCTGATGAAACGCTATGAGAACCTGGAGAACGAG 358  
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20  
QY 359 CTGATCTGCCCATCTGCTCTGAGATGTTTACCAAGCCTGTGTCATCTGCTGCCCA 418  
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
QY 419 CACAACTCTGCGGAAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTCGACC 478  
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60  
QY 479 AACCGGGTGGCTCAGTGTCCATGTCTGAGGTGCTTTCCTGCTGCTGCTGCTGCCCAT 538  
Db 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80  
QY 539 GAAGTGATCATGACCGGACCGGCTGACGGCTGACGGCTGACGAGAACCTGCTGTGGAAAAC 598  
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100  
QY 599 ATCATTTGACATCTACAAGCAGGAGTGTCTCCAGTCCGGCCCTGCAGAAAGCAGCCCG 658  
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120  
QY 659 ATGTGCAAGGAACACAGAGACGAGAGATCAACATCTACTGTCTACGTGTGAGGTGCT 718  
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
QY 719 ACTTCTCTCTCTGCAAGGTGTTTGGGCTCACCGGCTGAGGTGCTGCTGCTGCTGCTGCA 778  
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160  
QY 779 AGCATCTTCCAAAGGACAGAGACTGAGCTGAGTAACTATGTCATCTCCATGCTGCTGGGG 838  
Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGCACAGATCATCTCTAGCTGGAGGACTCTGTCAGAGTGAACCAAGGAG 898  
Db 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgArgValThrLysGlu 200  
QY 899 AATAGCCACCGGTGAAGGAGGAGCTGAGTCAAGAGTTTGGACACCTCTACGCCATCTCG 958  
Db 201 AsnSerHisGlnValGlyGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220  
QY 959 GATGAGAAGAGCGAGCTGCTGCGCGGATCATCGCAGGAGTACGCGAGGAGGAGGAGCTGGGC 1018

```

Db 221 AspGluLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuSer 240
Qy 1019 TTCATCGAGGCTCTGATCCTCCAGTACAGGAGGAGCTGGAAAGTCCACCAAGCTTCGTG 1078
Db 241 PheIleGluAlaLeuIleGlnGlnTyrglnGlnGluLeuAspLysSerThrLysLeuVal 260
Qy 1079 GAGACCGCCATCCAGTCCCTGATGAGCCGAGGGGTACTCTCTCAAGTGCCCAAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
Qy 1139 CAGCTCATCAGAGCAATGTAGACCTCCAGGCTCCAGGCTCCAGCTGGGAGACACAGCAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
Qy 1199 GCCTTTGAGACATCGACTACTTTACTCTGCACTTAGAACACATAGCAGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
Qy 1259 GCCATTGACTTTGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 4
Q6DE39 PRELIMINARY; PRT; 356 AA.
AC Q6DE39;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Rnf30-prov protein.
GN Name=rnf30-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_taxid=8355;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA "Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;

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RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; BC0077305; AAH77305.1; -
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR006058; 2Fe2S fd_BS.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00643; zf-B_box; 1.
DR SMART; SM00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 356 AA; 41097 MW; DC4F7B6655F5FD30 CRC64;

Alignment Scores:
Pred. No.: 3.13e-73 Length: 356
Score: 1188.50 Matches: 212
Percent Similarity: 82.78% Conservative: 62
Best Local Similarity: 64.05% Mismatches: 52
Query Match: 41.73% Indels: 5
DB: 2 Gaps: 2

US-10-775-649-5 (1-1597) x Q6DE39 (1-356)
Qy 299 ATGATTATATAATCTAGCTCTGATCTCTGATGGAACGCTATGGAGAACTCGAGAGCAG 358
Db 1 MetAspTyrAsnSerGluIleIleArgGluAsnAsnProMetAspSerLeuGluLysGln 20
Qy 359 CTGATCTGCCCCATCTGCTCGAGATGTTTACCAGCCTGTGGTCTCATCTGCGCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheAsnLysProValValIleLeuProCysGln 40
Qy 419 CACAACCTCTCGCGAGTGTGCCAACGACATCTTCAGGCTCGGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaGlyAsnProTyrTrpSer 60
Qy 479 AACCGCGTGGCTCAGTGTCCATGTCTGGAGTGTCTTCCGTTGCCCTCGTGGCGCCAT 538
Db 61 ThrArgSer-----SerValSerGlyArgPheArgCysProThrCysArgHis 77
Qy 539 GAAGTGTATGAGACCGGCGAGGGGTGTACGGCCTGCAGAGGAACTGCTGTGGAAAC 598
Db 78 GluValIleLeuAspArgHisGlyValTyrglyLeuGlnArgAsnLeuValGluAsn 97
Qy 599 ATCATTGACATCTCAGACGAGAGTGTCTCAGTGGCCCTTCGAGAAGAGCGACCCCG 658
Db 98 IleIleAspIleTyrLysGlnAspCysThrSerArgProGluLysLysGluAsnHisPro 117
Qy 659 ATGTGCAAGGAACAGCAGAGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT 718
Db 118 MetCysGluLysHisGluAspGluLysIleAsnIleTyrCysLeuSerCysGlnValAla 137
Qy 719 ACTTGCTCTTGTGCAAGGTGTTTGGGGCTCACCAGGCTGTGAGGTGGCCCTTTGCAA 778
Db 138 ThrCysSerMetCysLysValPheGlyValHisLysAspCysAspValSerProLeuGln 157
Qy 779 AGCATCTTCAAGGACAGACAGACTGAGTGTGAGTAAGTCACTCTCATCTGCTGTGGCGGG 838
Db 158 AsnValTyrGlnSerGlnLysThrGluLeuAsnSerSerIleSerMetLeuValAlaGly 177
Qy 839 AACGACCGAGTGCAGACCATCATCTCTCAGCTGGAGGACTCGTCAGAGTGCACCAAGAG 898
Db 178 AsnAspArgIleGlnCysIleLeuSerGlnLeuGluSerCysLysThrIleGlnGlu 197

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QY 899 AATAGCCACCAGCTGTAAGGAGGAGCTGAGTCAGACAGTTTGACACCCCTCTACGCCATCTTG 958
Db 198 AnSerLysSerLysLysGluHisValAnGluMetPheGluThrLeuSerArgCysLeu 217
QY 959 GATGAGAAGAAGCAGGAGCTGTGCGAGCGGATCCAGCAGAGCAGAGGAGAGCTGGGC 1018
Db 218 GluGluLysLysThrHisLeuValGlnGlnIleSerGlnAlaGluGluGluLysLeuAsn 237
QY 1019 TTCATCGAGGCTGTGATCTCCAGTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTGTG 1078
Db 238 IleValArgSerLeuIleValArgCysGlnGlnLeuGlnSerSerAsnGluLeu 257
QY 1079 GAGACCGCATCCAGTCCCTCGATGAGCCGAGGCGCTACCTTCCTCTCAAGTGCACAG 1138
Db 258 GlnAsnAlaPheGlnAlaMetGluGlnThrGlyProAlaAsnPheLeuLeuGluSerLys 277
QY 1139 CAGCTCATCAAGAGCATTAGAACGCTCCAGGGCTCCAGGCTGGCGGAGACAGAGCAA 1198
Db 278 GlnLeuIleLysLysLeuMetGluAlaSerLysGlyCysGlnLeuGluLysThrGluLeu 297
QY 1199 GCGTTTGACAACTGACTTACTCTGACTTAGACATAGACATAGCAGAGCGCTTGAGG 1258
Db 298 GlyPheGluAsnMetAspGlnPheThrLeuAspMetGluHisValSerGlnCysLeuArg 317
QY 1259 GCCATTGACTTTGGCAGAGTAAAGGATGTGAT 1291
Db 318 AsnIleAspPheSerAla-----AsnCysAsp 326

RESULT 5
ID Q8IUD9 PRELIMINARY; PRT; 540 AA.
AC Q8IUD9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RING finger protein 29.
GN Name=RNF29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Iakovenko A., Gautel M.;
RT "Titin-associated zinc-finger proteins link titin kinase to
RL transcriptional control.";
RL J. Muscle Res. Cell Motil. 21:833-833 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=22302063; PubMed=12414993;
RA Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,
RT Furst D.O., Karsenti E., Gautel M.;
RT "Transient association of titin and myosin with microtubules in
RL nascent myofibrils directed by the MURF2 RING-finger protein.";
RL J. Cell Sci. 115:4469-4482 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Gautel M.S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AJ431704; CAD24432.1;
DR GO: GO:0000151; Crubiquitin ligase complex; IEA.
DR GO: GO:0004842; Fubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F.zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR000315; Znf Bbox.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00643; zf-B_box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.

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DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00899; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 540 AA; 60245 MW; D16B7E06BF9C60A CRC64;

Alignment Scores:
Pred. No.: 6,43e-69 Length: 540
Score: 1126.50 Matches: 221
Percent Similarity: 67.00% Conservative: 45
Best Local Similarity: 55.67% Mismatches: 60
Query Match: 39.55% Indels: 71
DB: 2 Gaps: 2

US-10-775-649-5 (1-1597) x Q8IUD9 (1-540)
QY 80 ATGAGCAGCTTCTCTGAATTACAAGTCTTTCTTCCAAGAGCAGCAGCACCATGATTAATTG 139
Db 1 MetSerAlaSerLeuAsnTyrlsSerPheSerLysGluGlnThrMetAsp----- 18
QY 140 GAAAAGCAACTGATCTGTCCTCCATCTGCCTAGAGATGTTCCAGAACCTGTGTCTATCTC 199
Db 18 ----- 18
QY 200 CCTTGCAGCAGCAACCTGTGCAGGAAATGTGCGGGCCCCCTTGGAGACAAAGACTTGT 259
Db 18 ----- 18
QY 260 GTGACGCGAGTGGGCAAGACAGTCGCATTTCAAAGCAATATGATTAATAATCTAGCCTG 319
Db 18 ----- 18
QY 320 ATTCTGATGGAACGCTATGGAGAACCTGGAGAGACAGCTGATCTGCCCATCTCCCTG 379
Db 19 -----AsnLeuGluLysGlnLeuIleCysProIleCysLeu 30
QY 380 GAGATGTTTACCAAGCTGTGTCTCATCTCCCTGCAACACACAACTCTGCCGGAAGTGT 439
Db 31 GluMetPheThrLysProValValIleLeuProCysGlnHisAsnLeuCysArgLysCys 50
QY 440 GCCAACGACATCTTCCAGGCTCGAATCCCTACTCGAACCAACCGCGGTGGCTCAGTGTCC 499
Db 51 AlaSerAspIlePheGlnAlaSerAsnProTyLeuProThrArgGlyGlyThrThrMet 70
QY 500 ATGCTCTGAGGTGCTTTCCGTTGCCCTCGTCCCGCCATGAAGTATCATGACCGGCAC 559
Db 71 AlaSerGlyGlyArgPheArgCysProSerCysArgHisGluValValLeuAspArgHis 90
QY 560 GGGGTGTACGGCTGCAGAGAACCTGTGTGTGGAAAAACATCATTCACATCTACAAGCAG 619
Db 91 GlyValTyGlyLeuGlnArgAsnLeuLeuValGluAsnIleIleAspIleTyrlsGln 110
QY 620 GAGTGTCTCAGTCGGCCCTCGCAGAAAGCAGCCACCCGATGTGCAAGAAACACGAAGAC 679
Db 111 Glu---SerThrArgProGluLysLysSerAspGlnProMetCysGluGluHisGluGlu 129
QY 680 GAGAAATCAACATCTACTCTCTCAGTGTGAGTGGCTTCTTCTCTCTTGTGCAAGGTG 739
Db 130 GluArgIleAsnIleTyrlsCysLeuAsnCysGluValProThrCysSerLeuCysLysVal 149
QY 740 TTTGGGGCTCACGAGCCTGTGAGTGTGCCCTTTGCAAAAGCATCTTCCAAGACAGAAAG 799
Db 150 PheGlyAlaHisLysAspCysGlnValAlaProLeuThrHisValPheGlnArgGlnLys 169
QY 800 ACTGAGCTGAGTAATGATCTTCCATCTCCATGTGTGTGGGGGGAACGACCGATGCAGACATC 859
Db 170 SerGluLeuSerAspGlyIleAlaIleLeuValGlySerAsnAspArgValGlnGlyVal 189
QY 860 ATCTCTCAGCTGGAGGCTCGTGAGAGTGACCAAGGAGAATAGCCACCGGTGAGGAG 919
Db 190 IleSerGlnLeuGluAspThrCysLysThrIleGluGluCysCysArgLysGlnLysGln 209

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Db 230 ThrGlnValIleThrArgThrGlnGluGluLysLeuGluHisValArgAlaLeuIleLys 249  
QY 1040 CAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCCGATCCAGTCCCTG 1099  
Db 250 LysTyrSerAspHisLeuGluAenValSerLysLeuValGluSerGlyIleGlnPheMet 269  
QY 1100 GATGACCCGGAGGGCTACCTTCCTCAAGTGCCCAAGCAGCTCATCAAGAGCATTGTA 1159  
Db 270 AspGluProGluMetAlaValPheLeuGlnAenAlaLysThrLeuLeuLysIleSer 289  
QY 1160 GAAGCTCCAGGCTGCCAGCTGGGAGACAGACAAAGCTTTCAGAACATGGACTAC 1219  
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QY 1220 TTACTCTGGACTTAGAACACATAGCAGAGGCCCTTGAGGCCCATTCATT 1270  
Db 310 PheThrValAenLeuAenArgGluGluLysIleIleArgGluIleAaspPhe 326

RESULT 9

Q9ERP3 PRELIMINARY; PRT; 366 AA.  
AC Q9ERP3; 1110.00  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE RING-finger protein MURF.  
GN Name=Rnf30;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP "Regulation of microtubule dynamics and myogenic differentiation by  
RT MURF, a striated muscle RING-finger protein.";  
RL J. Cell Biol. 150:771-784 (2000).  
CC -I- SIMILARITY: Contains 1 RING-type zinc finger.  
DR EMBL; AF294790; AAG03076.1; -  
DR MGD; MG1:189623; Rnf30.  
DR GO; GO:0005875; C: microtubule associated complex; IDA.  
DR GO; GO:0008017; F: microtubule binding; IDA.  
DR GO; GO:0007026; P: microtubule stabilization; IDA.  
DR InterPro; IPR00315; Znf Bbox.  
DR InterPro; IPR001841; Znf ring.  
DR Pfam; PF00643; zf-B box; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00336; BBOX; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS00119; ZF BBOX; 1.  
DR PROSITE; PS00518; ZF RING 1; 1.  
DR PROSITE; PS00089; ZF RING 2; 1.  
KW Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 366 AA; 41130 MW; 6CD3429162D5BEFA CRC64;

Alignment Scores:

Pred. No.: 7.9e-68 Length: 366  
Score: 1110.00 Matches: 212  
Percent Similarity: 78.53% Conservative: 55  
Best Local Similarity: 62.35% Mismatches: 63  
Query Match: 38.97% Indels: 10  
DB: 2 Gaps: 3

US-10-775-649-5 (1-1597) x Q9ERP3 (1-366)

QY 278 ACAGTCGCATTTCAAGACATATGGATTATTAATCTAGCTGATTCCTGATGGAACGCT 337  
Db 4 ThrValGlyPheLys-----ProLeuLeuGlyAlaHisAen 16

QY 338 ATGGAGAACCTGGAGAACGAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCT 397  
Db 17 MetAspAenLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysPro 36  
QY 398 GTGGTCATCTCCTGCTGCCAACAACACCTCTCTGCCGGAAGTGTGCCAACACATCTTCCAG 457  
Db 37 ValValIleLeuProCysGlnHisAenLeuCysArgLysCysAlaAenAspValPheGln 56  
QY 458 GCTGGCAATCCCTACTTGGACCAACCGCGTGCTCAGTCTCCATGCTCTGGAGTCTGTTTC 517  
Db 57 AlaSerAenProLeuThrPglNserArgGlySerThrThrValSerSerGlyGlyArgPhe 76  
QY 518 CTTTGCCCTCTGCGCCCATGAAGTATCATCGACCGCGGCTGTACGCGCTCCAG 577  
Db 77 ArgCysProSerCysArgHisGluValValLeuAenAspArgHisGlyValTyrGlyLeuGln 96  
QY 578 AGAACCTCTCTGGTGGAAAAACATCTATTGACATCTACAGCAGAGTGTCTCCAGTCCGGCCC 637  
Db 97 ArgAenLeuValGluAenIleAspIleTyrLysGlnGlu---SerSerArgPro 115  
QY 638 CTG-----CAGAAAGGCGACCCCGATGTCACAGGAACACGACGAGAGATCAAC 691  
Db 116 LeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAenGluLysIleAen 135  
QY 692 ATCTACTGTCTCACGTGTGAGGTGCTCTACTTCTCTGCAAGGTGTTTGGGGCTCAC 751  
Db 136 IleTyrCysLeuSerCysGluValProThrCysSerLeuCysLysValPheGlyAlaHis 155  
QY 752 CAGGCTGTGAGGTGCTCCCTTTTGCACAGCATCTTCCAAAGGACAGAACTGAGCTGAGT 811  
Db 156 LysAspCysGluValAlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSer 175  
QY 812 AACTGCATCTCCATGCTGTGGTGGGAGACGACCGAGTCACAGCATCATCTCTCAGCTG 871  
Db 176 AspGlyIleAlaMetLeuValAlaGlyAenAspArgValGlnAlaValIleThrGlnMet 195  
QY 872 GAGGACTCTGTCAGAGTGCACCAAGGAGATATCCACAGGTGAAGGAGGAGCTGAGTCA 931  
Db 196 GluGluValCysGlnThrIleGluAenSerArgArgGlnLysGlnLeuLeuAenGln 215  
QY 932 AAGTTTGACACCTCTACGCCATCTCTGATGATGAGAGAGAGGAGCTGTCTGACGGGATC 991  
Db 216 ArgPheGluThrLeuCysAlaValLeuGluGluArgLysGlyGluLeuGlnAlaLeu 235  
QY 992 ACGCAGGAGCAGGAGGAGAGTGGGCTTCATCGAGGCTCTCATCTCCAGTACAGGGAG 1051  
Db 236 AlaArgGluGlnGluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAen 255  
QY 1052 CAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCTCCCTGGATGAGCCCGA 1111  
Db 256 HisLeuGluGlySerSerLysLeuValGluSerAlaIleGlnSerMetGluGluProGln 275  
QY 1112 GGGGTACCTCTCTCAAGTCCAGCAGCTCATCAAGAGCATTTAGAACCTTCAAG 1171  
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QY 1172 GCTGCCAGCTCGGGAAGACAGCAAGGCTTTGAGAACACTGACTACTTTACTCTGGAC 1231  
Db 296 ValGluLeuAlaGlyArgProGluProGlyTyrGluSerMetGluGlnPheSerValSer 315  
QY 1232 TTAGAACACATAGCAGAGCCCTTGAGGGCCATTGAGCTTTGGGACAGGTAAAGATGTGAT 1291  
Db 316 ValGluHisValAlaGluMetLeuArgThrIleAenPheGlnProGlyAlaAlaGlyAen 335  
RESULT 10  
RN29 HUMAN  
ID RN29 HUMAN STANDARD; PRT; 436 AA.  
AC Q9BYT6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE RING finger protein 29 (Muscle specific ring finger protein 2)  
DE (MURF2).





[illegible]



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 15, 2005, 14:22:31 ; Search time 36 Seconds  
(without alignments)  
6623.031 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 2848

Sequence: 1 ctcgagattacccttacag.....gaaataaattatctgtgcc 1597

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued\_Patents\_AA -QFMT=fastcan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10775649 @CGN 1.1.33 @runat\_14062005\_14111\_20695 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1802	63.3	343	US-09-908-988B-6	Sequence 6, Appli
2	1613	56.6	353	US-09-484-970B-171	Sequence 171, App
3	1114.5	39.1	545	US-09-908-988B-4	Sequence 4, Appli
4	1110	39.0	366	US-09-908-988B-2	Sequence 2, Appli
5	267.5	9.4	223	US-09-327-983-5	Sequence 5, Appli
6	257	9.0	435	US-09-561-989-10	Sequence 10, Appli
7	240	8.4	519	US-09-949-016-7883	Sequence 7883, Ap
8	237	8.3	513	US-09-949-016-10972	Sequence 10972, A
9	232.5	8.2	327	US-09-949-016-7575	Sequence 7575, Ap
10	223	7.8	842	US-09-949-016-7012	Sequence 7012, Ap
11	223	7.8	870	US-09-949-016-9625	Sequence 9625, Ap
12	221	7.8	413	US-09-663-600A-198	Sequence 198, App

ALIGNMENTS

RESULT 1

US-09-908-988B-6  
; Sequence 6, Application US/09908988B  
; Patent No. 6740751  
; GENERAL INFORMATION:  
; APPLICANT: OLSON, ERIC  
; APPLICANT: SPENCER, JEFFREY A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
; FILE REFERENCE: MYOG:028US  
; CURRENT APPLICATION NUMBER: US/09/908,988B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/219,020  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 343  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-908-988B-6

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Pred. No.:	1802.00	Matches:	343
Score:	100.00%	Conservative:	0
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Query Match:	63.27%	Indels:	0
DB:	4	Gaps:	0

US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)

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DB 1 MetAspTyrLysSerSerLeuileProaspGlyAenAlaMetGluashLeuGln 20





Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLysLeuSer 240  
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGGAGCAGCTGGAAAGCTCCACCAAGCTTG 1078  
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Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280  
QY 1139 CAGCTCATCAGAGCATTTAGAACGCTCCAGGGCTGCCAGCTGGGAAGACAGACAA 1198  
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
QY 1199 GCGTTTGAAACATGAGTACTTTACTCTGGACTTTAGAACACATAGCAGAGCCCTTGAGG 1258  
Db 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320  
QY 1259 GCCATTGATTTGGACA 1276  
Db 321 AlaIleAspPheGlyThr 326

## RESULT 3

US-09-908-988B-4

; Sequence 4, Application US/09908988B

; Patent No. 6740751

; GENERAL INFORMATION:

; APPLICANT: OLSON, ERIC

; APPLICANT: SPENCER, JEFFREY A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES

; FILE OF INVENTION: IN STRIATED MUSCLE CELLS

; FILE REFERENCE: MYOG:028US

; CURRENT APPLICATION NUMBER: US/09/908,988B

; CURRENT FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: 60/219,020

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 545

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-908-988B-4

## Alignment Scores:

Pred. No.:	28-100	Length:	545
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Percent Similarity:	66.75%	Conservative:	45
Best Local Similarity:	55.42%	Mismatches:	61
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US-10-775-649-5 (1-1597) x US-09-908-988B-4 (1-545)

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QY 140 GAAAGCAACTGATCTGTCCCATCTGCGCTAGAGATGTTCAAGACGCTGTGTCATCTC 199  
Db 18 ----- 18  
QY 200 CTTGCCAGCACAACTGTGCAGGAAATGTGCGGGCCCCCTTGGAGACAAAGACTTGT 259  
Db 18 ----- 18  
QY 260 GTGACGCGAGGTGGCAAGACAGTCCGATTTCAAAGCAATATGGAATTATAAATCTAGCCTG 319  
Db 18 ----- 18  
QY 320 ATTCTGTATGGAACGCTATGGAAGAACCTGGAGAACGAGCTGATCTGCCCATCTGCGCTG 379  
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Db 19 -----AsnLeuGluLysGlnLeuIleCysProIleCysLeu 30  
QY 380 GAGATGTTTACAAAGCCTGTGTCATCTGCGCTGCCAACACAACTCTGCGGGAAGTGT 439  
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QY 440 GCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGAACCAACCGCGGTGGCTCACTGTC 499  
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Db 130 GluArgIleAsnIleTyrlsCysLeuAsnCysGluValProThrCysSerLeuCysVal 149  
QY 740 TTTGGGCTCACAGGCTGTGAGGTGCTCCCTTTTGCAGAGCATCTTCAAGAGCAGAG 799  
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QY 1160 GAAGCTTCAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTTGAGAACATGACTATC 1219  
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## RESULT 4

US-09-908-988B-2

; Sequence 2, Application US/09908988B

; Patent No. 6740751

; GENERAL INFORMATION:

; APPLICANT: OLSON, ERIC

; APPLICANT: SPENCER, JEFFREY A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES

; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS

; FILE REFERENCE: MYOG:028US

; CURRENT APPLICATION NUMBER: US/09/908,988B

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; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-908-988B-2

Alignment Scores:
Pred. No.: 4,4e-100 Length: 366
Score: 1110.00 Matches: 212
Percent Similarity: 78.53% Conservative: 55
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QY 398 GTGGTCATCTGCTGCCAACAACACCTCTGCCGGAAGTGTGCCAACACATCTTCCAG 457
Db 37 ValValIleLeuProCysGlnHisAenLeuCysArgLysCysAlaAsnAspValPheGln 56
QY 458 GCTGCCAATCCCTACTGGACCAACCGCGGTGCTCAGTCTCCTGAGGTGCTTTC 517
Db 57 AlaSerAsnProLeuTrpGlnSerArgGlySerThrValSerSerGlyGlyArgPhe 76
QY 518 CGTTGCCCTCTGTCGCCCATGAAGTGATCATGGACCGGCACGGGTGTACGGCTCGCAG 577
Db 77 ArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrglyLeuGln 96
QY 578 AGAACTCTGCTGTGGAACATCATATGATCATCTACAAGCAGAGTGTCCAGTGGGCC 637
Db 97 ArgAsnLeuLeuValGluAsnIleIleAspIleTyrglyLysGlnGlu---SerSerArgPro 115
QY 638 CTG-----CAGAAAGCGACCCCGCATGTGCAAGGAACAGACGAGAGATCAAC 691
Db 116 LeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAen 135
QY 692 ATCTACTGTCTCACGTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGTTTGGGGCTCAC 751
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; Patent No. 6633819
; GENERAL INFORMATION:
; APPLICANT: Rzhetsky, Andrey
; TITLE OF INVENTION: GENE DISCOVERY THROUGH COMPARISONS OF
; TITLE OF INVENTION: NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG
; FILE OF INVENTION: GENES AND PROTEINS
; FILE REFERENCE: AP31869 070050.1046
; CURRENT APPLICATION NUMBER: US/09/327,983
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-327-983-5

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US-10-775-649-5 (1-1597) x US-09-327-983-5 (1-223)
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Db 22 ArgVal---LeuProCysSerHisAsnPheCysLysLysCysLeuGluGlyIleLeuGlu 40
QY 458 GCTGGGAATCCCTACTGGACCAACCGCGGTGCTCAGTGTCTCCTGAGGTGCT--- 514
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QY 515 -----TTCCGTTGCCCTCTGTCGCCCATGATGATGATCATGACCGGACCGGGGTGTAC 568
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QY 569 GGCCTGCAGAGAACTGCTGCTGGGAAAACATCATTGACATCTACAAGCAGGAGTCTCC 628
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QY 629 AGTCGGCCCTCGCAAGAGCGACCCCGATGTGCAAGAAACACGAAACAGAGAGATC 688
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GenCore version 5.1.6  
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SUMMARIES

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ALIGNMENTS

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; Patent No. US20020127690A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSON, ERIC  
; APPLICANT: SPENCER, JEFFREY A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS  
; FILE REFERENCE: MYOG:028US  
; CURRENT APPLICATION NUMBER: US/09/908,988B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/219,020  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 343  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-09-908-988B-6									
Alignment Scores:									
Pred. No.:	2.97e-131	Length:	343						
Score:	1802.00	Matches:	343						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	63.27%	Indels:	0						
DB:	9	Gaps:	0						
US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
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DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACAAAGCCTGTGTATCTCGCTCCCA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGAGTGTCCAAAGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60						
QY	479	AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyIleArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCGGTGTACGGCTGTCAGAGAACCTGCTGGTGGAAAAAC	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAAGCAGGAGTCTCCAGTCCGCCCCTGCAGAAAGCAGCACCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTCCAGGAACACGAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCAAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCAAAGCAGAGACTGAGTCACTGAGTAACTGCATCTCCATCTCGTGGCGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACACCATCATCTCTCAGCTGAGGACTCTGTCAGAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTGCAGCGGATCACGACGAGACGAGGAGAGACTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuGly	240						
QY	1019	TTCATTCGAGGCTCATCTCCTCCAGTACAGGACGAGCTGGAAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACTTCTCTCAAGTGCCTAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAAAGGCTGCCAGCTGGGGAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTTGAGAACATGGACTACTTTTACTCTGACTTTAGAACACATACGAGAGGCTTGAGG	1258						

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DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACAAAGCCTGTGTATCTCGCTCCCA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGAGTGTCCAAAGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60						
QY	479	AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyIleArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCGGTGTACGGCTGTCAGAGAACCTGCTGGTGGAAAAAC	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAAGCAGGAGTCTCCAGTCCGCCCCTGCAGAAAGCAGCACCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTCCAGGAACACGAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCAAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCAAAGCAGAGACTGAGTCACTGAGTAACTGCATCTCCATCTCGTGGCGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACACCATCATCTCTCAGCTGAGGACTCTGTCAGAGTGCACCAAGGAG	898						
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QY	899	AATAGCCACAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTGCAGCGGATCACGACGAGACGAGGAGAGACTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuGly	240						
QY	1019	TTCATTCGAGGCTCATCTCCTCCAGTACAGGACGAGCTGGAAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACTTCTCTCAAGTGCCTAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAAAGGCTGCCAGCTGGGGAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTTGAGAACATGGACTACTTTTACTCTGACTTTAGAACACATACGAGAGGCTTGAGG	1258						

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US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCATGGAACCGCTATGGAGAACCTGGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACAAAGCCTGTGTATCTCGCTCCCA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGAGTGTCCAAAGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
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QY	479	AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyIleArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCGGTGTACGGCTGTCAGAGAACCTGCTGGTGGAAAAAC	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
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DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTCCAGGAACACGAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCAAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCAAAGCAGAGACTGAGTCACTGAGTAACTGCATCTCCATCTCGTGGCGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACACCATCATCTCTCAGCTGAGGACTCTGTCAGAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTGCAGCGGATCACGACGAGACGAGGAGAGACTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuGly	240						
QY	1019	TTCATTCGAGGCTCATCTCCTCCAGTACAGGACGAGCTGGAAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACTTCTCTCAAGTGCCTAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAAAGGCTGCCAGCTGGGGAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTTGAGAACATGGACTACTTTTACTCTGACTTTAGAACACATACGAGAGGCTTGAGG	1258						

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Query Match:	63.27%	Indels:	0						
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QY	299	ATGGATTATAAATCTAGCCTGATTCTCATGGAACCGCTATGGAGAACCTGGAGAACGAC	358						
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QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACAAAGCCTGTGTATCTCGCTCCCA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGAGTGTCCAAAGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60						
QY	479	AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyIleArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCGGTGTACGGCTGTCAGAGAACCTGCTGGTGGAAAAAC	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAAGCAGGAGTCTCCAGTCCGCCCCTGCAGAAAGCAGCACCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTCCAGGAACACGAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCAAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCAAAGCAGAGACTGAGTCACTGAGTAACTGCATCTCCATCTCGTGGCGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACACCATCATCTCTCAGCTGAGGACTCTGTCAGAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTGCAGCGGATCACGACGAGACGAGGAGAGACTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuGly	240						
QY	1019	TTCATTCGAGGCTCATCTCCTCCAGTACAGGACGAGCTGGAAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACTTCTCTCAAGTGCCTAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAAAGGCTGCCAGCTGGGGAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
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US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCATGGAACCGCTATGGAGAACCTGGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACAAAGCCTGTGTATCTCGCTCCCA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGAGTGTCCAAAGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60						
QY	479	AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyIleArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCGGTGTACGGCTGTCAGAGAACCTGCTGGTGGAAAAAC	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAAGCAGGAGTCTCCAGTCCGCCCCTGCAGAAAGCAGCACCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTCCAGGAACACGAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
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QY	839	AACGACCGAGTGCACACCATCATCTCTCAGCTGAGGACTCTGTCAGAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
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DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
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QY	1079	GAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACTTCTCTCAAGTGCCTAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLe							

Db	301	GlyPheGluAsnMetAspTyrPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg	320	
QY	1259	GCCATTGACTTTGGGACAGGTAAAGATGTGATGTTTACATGTTTGACCTTTGAAAGGCAG	1318	
Db	321	AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln	340	
QY	1319	CGTTCTCTCT	1327	
Db	341	ArgSerSer	343	
RESULT 2				
US-10-775-649-6				
; Sequence 6, Application US/10775649				
; Publication No. US20040132160A1				
; GENERAL INFORMATION:				
; APPLICANT: OLSON, ERIC				
; APPLICANT: SPENCER, JEFFREY A.				
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES				
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS				
; FILE REFERENCE: MYOG-028USD2				
; CURRENT APPLICATION NUMBER: US/10/775,649				
; CURRENT FILING DATE: 2004-02-10				
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; NUMBER OF SEQ ID NOS: 6				
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QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACAAAGCCTGTGTGTATCTCTGCCCTGCGCAA	418	
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QY	479	AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTCCGCCCAT	538	
Db	61	AsnArgGlyGlySerValSerMetSerGlyIleArgPheArgCysProSerCysArgHis	80	
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QY	599	ATCATTGACATCTACAAGCAGGAGTGTCTCCAGTCGGCCCTCGAGAAAGCCACCCG	658	
Db	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120	
QY	659	ATGTCCAGGAACACGACGACGAGATCAACATCTACTGTCTCACGTGTGAGGTGCCT	718	
Db	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140	

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Db 181 AenAspArgValGlnThrIleLeuSerGlnLeuGluAspSerCysArgValThrLysGlu 200
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Db 201 AenSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGAGAGAGTGTCTGAGCGGATCAGCAGGAGTGAAGTGAAGTGAAGTGAAG 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuGly 240
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCGAGTGGAAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGGCATCCAGTCCCTGATGAGCCGAGGCGGAGTACCTTCTCAGTGCCTAAG 1138
Db 261 GlnThrAlaIleGlnLeuLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 280
QY 1139 CAGCTCATCAGAGCATTTAGAACCTCCAGGCTGCCAGTGGGGAAGACAGACGAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGAAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGGCTTGAGG 1258
Db 301 GlyPheGluAenMetAspTyPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGACAGGTAAGAGTGTGATGATGATGATGATGATGATGATGATGAT 1318
Db 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340
QY 1319 GCTTCCCTCT 1327
Db 341 ArgSerSer 343
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RESULT 3
; Sequence 6 Application US/10775627
; Publication No. US20040142446A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR FILING DATE: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR FILING DATE: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-775-627-6
Alignment Scores:
Pred. No.: 2,97e-131 Length: 343
Score: 1802.00 Matches: 343
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 63.27% Indels: 0
DB: 16 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-775-627-6 (1-343)
QY 299 ATGATTTAATAATCTAGCTGATTCCTGATGAAACGCTATGAGAACTCGAGAACCTGGAAGCAG 358
Db 1 MetAspTyLysSerSerLeuIleProAspGlyAenAlaMetGluAenLeuGlnLysGln 20
QY 359 CTGATCTCCCCCATCTGCTGAGATGTTTACCAAGCCTGTGGTTCATCTGCTGCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACTCTCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTTACTGGACC 478
Db 41 HisAenLeuCysArgLysCysAlaAenAspIlePheGlnAlaAaAenProTyTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGCTCGAGGTGCTTTCCTGCTGCCCTCGTGGCGCCAT 538
Db 61 AenArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGGACCGGCGGTGTACGCGCTGCAGAGAACCTGCTGTGGAAGAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyArgLysGlnArgAenLeuValGluAen 100
QY 599 ATCATTGACATCTACAGCAGAGTGTCCAGTGGCGCCCTGCAGAAAGGACGACCCG 658
Db 101 IleIleAspIleTyLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTCAGAGACAGACAGAGACGAGNAGATCAACATCTACTGTCTCAGCTGAGGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAenIleTyCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTTGTGCAAGTGTTTGGGGCTACCAAGGCTGTGAGGTGGCCCTTTGCAA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTGCATCTCCATCTGTTGGCGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAenCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGAGAGTGAAGCAGGAG 898
Db 181 AenAspArgValGlnThrIleLeuSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 958
Db 201 AenSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGAGAGAGTGTCTGAGCGGATCAGCAGGAGTGAAGTGAAGTGAAGTGAAG 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuGly 240
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCGAGTGGAAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGGCATCCAGTCCCTGATGAGCCGAGGCTGCCAGTGGGGAAGACAGACGAA 1138
Db 261 GlnThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys 280
QY 1139 CAGCTCATCAGAGCATTTAGAACCTCCAGGCTGCCAGTGGGGAAGACAGACGAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGAAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGGCTTGAGG 1258
Db 301 GlyPheGluAenMetAspTyPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGACAGGTAAGAGTGTGATGATGATGATGATGATGATGATGATGAT 1318
Db 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340
QY 1319 GCTTCCCTCT 1327
Db 341 ArgSerSer 343
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QY 1319 CGTCTCTCT 1327
Db 341 ArgSerSer 343

RESULT 4
US-10-061-043A-21
; Sequence 21, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-061-043A-21

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 14 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-061-043A-21 (1-351)

QY 299 ATGGATTATAATCTAGCTGATCTCTGATGAAACGCTATGAGAACCTGAGAAAGCAG 538
Db 1 MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20

QY 359 CTGATCTGCCCATCTGCTGAGAGTGTACCAAGCCTGTGCTATCTGCGCCGCCAA 418
Db 21 LeuileCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40

QY 419 CACAACCTCTGCCGGAAGTGTGCCAACGACATCTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60

QY 479 ACCCGGGTGGCTCAGTGTCCATGTCTGAGGTGCTTTCCGTTGCCCTCGTGGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80

QY 539 GAAGTCATCATGACCGGCACGGGGGTACGGCTCGCAGAGGAACCTGCTGGTGAAGAAC 598
Db 81 GluValIleWecAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100

QY 599 ATCATTGACATCTACAAGCAGGAGTGTCTCCAGTGGCCCTCGCAGAAAGCCAGCCCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120

QY 659 ATGTGAAGAACACAGACAGCAGAGATCAACATCTACTGTCTCAGCTGAGGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140

QY 719 ACTTGCTCTGTGCAAGGTGTTGGGCTCACAGCGCTGTGAGGTGCCCTTTGCAA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160

QY 779 AGCATCTTCAAGGACAGAAGACTGAGCTGAGTAATCGCATCTCCATGCTGTGGCGGG 838
Db 1 MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20

Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AAGCAGCCAGTGCAGACGATCATCTCTAGCTGGAGGACTCTGTCAGAGTGACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCCAGGTGAAGGAGGAGCTGAGTCAGAGTTTGTACACCCCTCTACGCCATCTCG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGACAGCGAGCTGCTGAGCGGATCACGACAGCAGCAGGAGAGCTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuAsp 240
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGGAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCCATCCAGTCCCTGATGAGCCGAGGGGCTACCTTCCTCTCAAGTGCACAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGACGATTTAGAAGCCTCCAAGGCTGCCAGCTGGGGAAGACAGACAA 1198
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGAAACATGAGCTACTTTACTCTGGACTTAGAACACATAGCAGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 5
US-10-061-043A-36
; Sequence 36, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-061-043A-36

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 14 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-061-043A-36 (1-351)

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Db 1 MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20

QY 359 CTGATCTGCCCATCTGCTGAGAGTGTACCAAGCCTGTGCTATCTGCGCCGCCAA 418
Db 21 LeuileCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40

QY 419 CACAACCTCTGCCGGAAGTGTGCCAACGACATCTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60

QY 479 ACCCGGGTGGCTCAGTGTCCATGTCTGAGGTGCTTTCCGTTGCCCTCGTGGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80

QY 539 GAAGTCATCATGACCGGCACGGGGGTACGGCTCGCAGAGGAACCTGCTGGTGAAGAAC 598
Db 81 GluValIleWecAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100

QY 599 ATCATTGACATCTACAAGCAGGAGTGTCTCCAGTGGCCCTCGCAGAAAGCCAGCCCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120

QY 659 ATGTGAAGAACACAGACAGCAGAGATCAACATCTACTGTCTCAGCTGAGGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140

QY 719 ACTTGCTCTGTGCAAGGTGTTGGGCTCACAGCGCTGTGAGGTGCCCTTTGCAA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160

QY 779 AGCATCTTCAAGGACAGAAGACTGAGCTGAGTAATCGCATCTCCATGCTGTGGCGGG 838
Db 1 MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
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QY 359 CTGATCTCCCATCTGCTGGAGATGTTTACCAAGCCTGTGGTCACTCTGCGCCCTGCCAA 418
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACACCTCTCCGCAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGCC 478
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCCCGTGGCTCAGTGTCCATGTCTGAGAGTCTTCCGTTGCGCCCTCTGCGCCGCAAT 538
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 61 AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGGACCGGCTGACGCGCTGACAGAGAACTGCTGTGGTGAAGAAC 598
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGATCATGACCGGACCGGCTGACGCGCTGACAGAGAACTGCTGTGGTGAAGAAC 658
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGACACGAGACGAGAGATCAACATCTACTGTCTCACGCTGTGAGGTGCT 718
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 121 MetCysLysGluHisGluAspGlyValTyrGlyLeuGlnArgAsnLeuValGluPro 140
QY 719 ACTTCTCTCTGTGCAAGGTGTTTGGGCTCACAGGCTGTGAGGTTGCCCTTTGCCAA 778
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACGAGTGTGCTGAGTAACTGATCTTCCATCTCTGCTGTGGTGGCGGG 838
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCTCTCAGCTGGAGGACTCTGTGAGGAGTGTGAGGTTGCC 898
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 958
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 201 AsnSerHisGlnValLysGlnGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln 240
QY 1019 TTCATCTGAGGCTCTGATCTCTCCAGTACAGGAGAGAGTGTGAAAGTCCACCAAGCTTGTG 1078
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 241 PheIleGluAlaLeuIleLeuGlnTyrArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260
QY 1079 GAGACCGCCCATCCAGTCTCCATGAGGCGGCGGCTTACCTTCTCTCAAGTCCCAAG 1138
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 261 GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGACATGTAGAGCTTCCAGGCTGCGAGGCTGCGAGGCTGCGAGGCTGCGAG 1198
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGlnGln 300
QY 1199 GCCTTTGAGACATGAGTCTTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1258
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db |||||||CysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 321 AlaIleAspPheGlyThr 326
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## RESULT 6

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US-10-061-043A-45
; Sequence 45, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
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; CURRENT APPLICATION NUMBER: US/10/061.043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-061-043A-45

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 14 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-061-043A-45 (1-351)
QY 299 ATGGATTATAATCTAGCTCTGATTCCTGATGAAACGCTATGGAGAACTCTGGAGAGCAG 358
Db |||||||MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCCATCTGCTCGAGATGTTTACCAAGCTGTGGTCACTCTGCGCCCTGCCAA 418
Db |||||||LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACTCTCCGCGAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGCC 478
Db |||||||HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGAGGACTCTTCCGTTGCGCCCTCTGCGCCGCAAT 538
Db |||||||AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGGACCGGCTGACGCGCTGACAGAGAACTGCTGTGGTGAAGAAC 598
Db |||||||GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGATCATGACCGGACCGGCTGACGCGCTGACAGAGAACTGCTGTGGTGAAGAAC 658
Db |||||||IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGACACGAGACGAGAGATCAACATCTACTGTCTCACGCTGTGAGGTGCT 718
Db |||||||GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuLeuSerAlaLys 280
QY 719 ACTTCTCTCTGTGCAAGGTGTTTGGGCTCACAGGCTGTGAGGTTGCCCTTTGCCAA 778
Db |||||||MetCysLysGluHisGluAspGlyValTyrGlyLeuGlnArgAsnLeuValGluPro 140
QY 779 AGCATCTTCCAGGACGAGTGTGCTGAGTAACTGATCTTCCATCTCTGCTGTGGTGGCGGG 838
Db |||||||SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCTCTCAGCTGGAGGACTCTGTGAGGAGTGTGAGGTTGCC 898
Db |||||||AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 958
Db |||||||AsnSerHisGlnValLysGlnGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018
Db |||||||AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln 240
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QY 1019 TTATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078
Db 241 PheileGluAlaLeulleuGlnTyrArgGluGlnLeuGlySerThrLysLeuVal 260
QY 1079 GAGACCGCATCAGTCCCTGGATAGCCGCGAGGGCTACCTCTCTCAAGTGCACAG 1138
Db 261 GluThrAlaileGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAGAGCATCTAGAGCTCCAGGGCTCCAGGGTGCAGCTGGGAGACAGACAA 1198
Db 281 ProLeulleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGAGAACATGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaileAspPheGlyThr 326

RESULT 7
US-10-061-043A-46
; Sequence 46, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; TYPE: PRT
; ORGANISM: rat
US-10-061-043A-46

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 14 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-061-043A-46 (1-351)
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Db 1 MetAspTyrLysSerGlyLeulleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCGTGTGTCATCTGCCCTGCCAA 418
Db 21 LeulleCysProilleCysLeuGluMetPheThrLysProValValilleLeuProCysGln 40
QY 419 CACACCTCTGCGGAGGTGCCACGACATCTCCAGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCCGGGTGGCTCAGTGTCCATGTCTGGAGGTGTTCCGTTGCCCTCGTGGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTATCATGACCGGCACGGGGGTGTACGGCTTCAGAGGAACTGCTGTGTGGAAC 598
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; ORGANISM: rat					
US-10-061-043A-47					
Alignment Scores:					
Pred. No.:	4-6e-121	Length:	351		
Score:	1671.00	Matches:	319		
Percent Similarity:	98.16%	Conservative:	1		
Best Local Similarity:	97.85%	Mismatches:	6		
Query Match:	58.67%	Indels:	0		
DB:	14	Gaps:	0		
US-10-775-649-5 (1-1597) x US-10-061-043A-47 (1-351)					
QY	299	ATGGATTATAATCTAGCTGATCTCTGATGAACCGCTATCGAGAACCTGAGAACGAC	358		
Db	1	MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluysGln	20		
QY	359	CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAA	418		
Db	21	LeuileCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40		
QY	419	CACAACTCTGCCGAAGTGTCCACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478		
Db	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60		
QY	479	AACCCGGTGGCTCAGTGTCCATGTCTGAGGTGCTTCCGTTGCCCTCGTCCGCCAT	538		
Db	61	AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis	80		
QY	539	GAAGTGATCATGGACCGGCAGCGGTGTACGCGCTGCAGAGGACCTCTGTGGAAC	598		
Db	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100		
QY	599	ATCATTGACATCTACAAGCAGGAGTGTCTCAGTCCGCGCCCTGCAGAAAGGACGACCCG	658		
Db	101	IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120		
QY	659	ATGTCAAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTCACGTGTGAGGTGCCT	718		
Db	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140		
QY	719	ACTTGCTCTCTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGTTCCTCCCTTTGCNA	778		
Db	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160		
QY	779	AGCATCTTCAAGGACAGAAGACTGAGCTGAGTAAGTCACTGCTCACTGTGTGAGGTGC	838		
Db	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180		
QY	839	AACGACCGAGTGCAGCATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGCACCAAGGAG	898		
Db	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200		
QY	899	AATAGCCACAGTGAAGAGAGCTGAGTCAAGATTGTGACACCTCTACGCCATCTCTG	958		
Db	201	AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu	220		
QY	959	GATGAGAACAAGCGAGCTGTGACAGCGGATCACGACGAGCAGGAGGAGGAGCTGGC	1018		
Db	221	AspGluLysSerGlnLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnLysLeuAsp	240		
QY	1019	TTTCATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTCGAAAGTCCACCAAGCTTGTG	1078		
Db	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260		
QY	1079	GAGACCCCATTCAGTCTCTGATGAGCCCGAGGGGCTACTCTCTCAAGTGCACAG	1138		
Db	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys	280		
QY	1139	CAGCTCATCAAGGACATTCAGACCTCCAGGGCTGCCAGCTGGGGAAGACAGACGA	1198		
Db	281	ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300		

QY	1199	GGCTTTGAGAACATCGGACTACTTACTCTGGACTTAGAACACATAGCAGAGCCTTGAGG	1255
Db	301	GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg	320
QY	1259	GCCATTGACTTTGGGACA	1276
Db	321	AlaIleAspPheGlyThr	326
RESULT 9			
US-10-060-634C-21			
; Sequence 21, Application US/10060634C			
; Publication No. US20030219739A1			
; GENERAL INFORMATION:			
; APPLICANT: Glass, David			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES			
; FILE REFERENCE: REG 753A			
; CURRENT APPLICATION NUMBER: US/10/060,634C			
; CURRENT FILING DATE: 2002-01-30			
; PRIOR APPLICATION NUMBER: 60/338,742			
; PRIOR FILING DATE: 2001-10-22			
; PRIOR APPLICATION NUMBER: 60/311,697			
; PRIOR FILING DATE: 2001-08-10			
; PRIOR APPLICATION NUMBER: 60/264,926			
; PRIOR FILING DATE: 2001-01-30			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 21			
; LENGTH: 351			
; TYPE: PRT			
; ORGANISM: rat			
US-10-060-634C-21			
Alignment Scores:			
Pred. No.:	4-6e-121	Length:	351
Score:	1671.00	Matches:	319
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	97.85%	Mismatches:	6
Query Match:	58.67%	Indels:	0
DB:	15	Gaps:	0
US-10-775-649-5 (1-1597) x US-10-060-634C-21 (1-351)			
QY	299	ATGGATTATAATCTAGCTGATCTCTGATGAACCGCTATCGAGAACCTGAGAACGAC	358
Db	1	MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluysGln	20
QY	359	CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAA	418
Db	21	LeuileCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40
QY	419	CACAACTCTGCCGAAGTGTCCACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478
Db	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60
QY	479	AACCCGGTGGCTCAGTGTCCATGTCTGAGGTGCTTCCGTTGCCCTCGTCCGCCAT	538
Db	61	AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis	80
QY	539	GAAGTGATCATGGACCGGCAGCGGTGTACGCGCTGCAGAGGACCTCTGTGGAAC	598
Db	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100
QY	599	ATCATTGACATCTACAAGCAGGAGTGTCTCAGTCCGCGCCCTGCAGAAAGGACGACCCG	658
Db	101	IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
QY	659	ATGTCAAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTCACGTGTGAGGTGCCT	718
Db	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140
QY	719	ACTTGCTCTCTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGTTCCTCCCTTTGCNA	778
Db	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160
QY	779	AGCATCTTCAAGGACAGAAGACTGAGCTGAGTAAGTCACTGCTCACTGTGTGAGGTGC	838
Db	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180
QY	839	AACGACCGAGTGCAGCATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGCACCAAGGAG	898
Db	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200
QY	899	AATAGCCACAGTGAAGAGAGCTGAGTCAAGATTGTGACACCTCTACGCCATCTCTG	958
Db	201	AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu	220
QY	959	GATGAGAACAAGCGAGCTGTGACAGCGGATCACGACGAGCAGGAGGAGGAGCTGGC	1018
Db	221	AspGluLysSerGlnLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnLysLeuAsp	240
QY	1019	TTTCATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTCGAAAGTCCACCAAGCTTGTG	1078
Db	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260
QY	1079	GAGACCCCATTCAGTCTCTGATGAGCCCGAGGGGCTACTCTCTCAAGTGCACAG	1138
Db	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys	280
QY	1139	CAGCTCATCAAGGACATTCAGACCTCCAGGGCTGCCAGCTGGGGAAGACAGACGA	1198
Db	281	ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300

Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
QY 779 AGCATCTTCCAAGGACAGAGACTGAGTAACTGCATCTCCATCTGCTGGCGGG 838  
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGACAGCATCTCTCAGCTGGAGACTCGTGACAGAGTGACCAAGGAG 898  
Db 181 AsnAspArgValGlnThrIleLeuSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
QY 899 AATAGCCACAGGTGAAGGAGAGCTGAGTCAGAGTTTGACACCTCTACGCCATCTCTG 958  
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyAlaIleLeu 220  
QY 959 GATGAAAGAACCGAGCTGCTGCAGCGGATCCACGAGGAGCAGGAGAGCTGGGC 1018  
Db 221 AspGluLysSerGlnLeuGlnArgGileThrGlnGluGlnGluLysLeuAsp 240  
QY 1019 TTCATCGAGGCTCGATCTCCAGTACAGGAGCAGCTGAAAAGTCCACCAAGCTTGTG 1078  
Db 241 PheIleGluAlaLeuIleLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 260  
QY 1079 GAGACCGCATCCAGTCCCTGGATAGCCCGAGGGGCTACCTTCTCTCAAGTGCAG 1138  
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280  
QY 1139 CAGCTCATCAAGAGCATTGAGAAGCTCCAAAGGCTCCAGGGCTGCAGTGGGGAAGCAGACAA 1198  
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
QY 1199 GGCTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGAGG 1258  
Db 301 GlyPheGluAsnMetAspTyPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320  
QY 1259 GCCATTGACTTTGGGACA 1276  
Db 321 AlaIleAspPheGlyThr 326

RESULT 10  
US-10-060-634C-36  
; Sequence 36, Application US/10060634C  
; Publication No. US20030219739A1  
; GENERAL INFORMATION:  
; APPLICANT: Glass, David  
; APPLICANT: Bodine, Sue  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES  
; FILE REFERENCE: REG 753A  
; CURRENT APPLICATION NUMBER: US/10/060,634C  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: 60/338,742  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/311,697  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/264,926  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: rat  
US-10-060-634C-36

Alignment Scores:  
Pred. No.: 4,6e-121 Length: 351  
Score: 1671.00 Matches: 319  
Percent Similarity: 98.16% Conservative: 1  
Best Local Similarity: 97.85% Mismatches: 6  
Query Match: 58.67% Indels: 0  
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-060-634C-36 (1-351)

QY 299 ATGGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGAGAACCTTGAGAGACGAG 358  
Db 1 MetAspTyLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20  
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACAGACCTGTGGTCTATCTCTGCCCTCCCAA 418  
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
QY 419 CACAACTCTCGCGGAAGTGCACACGACATCTTCCAGGCTGCGAATCCCTACTCTGACC 478  
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyTrpThr 60  
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCTGTTTCCGTTGCCCTCGTCCGCCCAT 538  
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80  
QY 539 GAAGTGATCATGGACCGGCACCGGGTGTACGGCTTCAGAGAACCTGTGTGTGGAAAC 598  
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QY 599 ATCATGTGACATCTACAAGCAGGAGTCTCCAGTCCGCCCTGCAGAAAGCGACCCCG 658  
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QY 659 ATGTGCAAGAAACACCAAGACGAGAGATCAACATCTACTGTCTCACTGTGTGAGGTGCCT 718  
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyLysLeuThrCysGluValPro 140  
QY 719 ACTTGCTCTTGTGCAGGTGTTGGGCTCACAGGCCCTGTGAGGTGCCCTCTTTGCCAA 778  
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
QY 779 ASCATCTTCCAAGGACAGAGACTGAGCTGAGTAACTGCATCTCCATGTGTGTGGCGGG 838  
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGACAGAGTGACCAAGGAG 898  
Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
QY 899 AATAGCCACCGGTGAAGGAGGAGCTGAGTGAAGTTTGACACCTCTACGCCATCTCTG 958  
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyAlaIleLeu 220  
QY 959 GATGAAAGAACCGAGCTGCTGCAGCGGATCCACGAGGAGCAGGAGAGCTGGGC 1018  
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QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGAAAAGTCCACCAAGCTTGTG 1078  
Db 241 PheIleGluAlaLeuIleLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 260  
QY 1079 GAGACCGCATCCAGTCCCTGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCAG 1138  
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280  
QY 1139 CAGCTCATCAAGAGCATTGAGAAGCTCCAAAGGCTGCAGCTGGGGAAGCAGACAA 1198  
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
QY 1199 GGCTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGAGG 1258  
Db 301 GlyPheGluAsnMetAspTyPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320  
QY 1259 GCCATTGACTTTGGGACA 1276  
Db 321 AlaIleAspPheGlyThr 326

RESULT 11  
US-10-060-634C-45  
; Sequence 45, Application US/10060634C  
; Publication No. US20030219739A1  
; GENERAL INFORMATION:

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; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 45
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-060-634C-45
Alignment Scores:
Pred. No.: 4.6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 15 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-060-634C-45 (1-351)
QY 299 ATGGATTATAATCTAGCTGATTCCTGATGAACGCTATGGAACCTGAGAACCTGGAAGCAG 358
DB 1 MetAspTyrLysSerGlyLeuLeuProAspGlyAsnAlaMetGluAsnLeuGluysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCTGCCCTGCCAA 418
DB 21 LeuileCysProileCysLeuGluMetPheThrLysProValValleuProCysGln 40
QY 419 CACAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTCGCAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGGTGGCTAGTGTCCATGTCTGGAGTGTGTTCCGTTGCTGCTGCTGCGCCCAT 538
DB 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGGACCGGGTGTACGCCCTGCAGAGCACTGCTGTGTGGAAC 598
DB 81 GluValIleMeAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTGTCTCCAGTCCGCCCTCCAGAAAGCGCACCCG 658
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QY 659 ATGTGGAAGGAACAGCAAGACAGAGATCAATCTACTGTCTCAGCTGTGAGTGTGCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
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DB 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
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DB 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValalagly 180
QY 839 AACGACCGAGTGCAGCATCATCTCTCAGCTGAGGACTCTGTGAGAGTACCAGGAG 898
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1019 TTCATCGAGGCTCTGATCCTCCAGTACAGGAGGAGCTGGAAAGTCCACCAAGCTTGTG 1078
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1079 GAGACCGCATCCAGTCTCCCTGGATGAGCCGCGAGGGGCTTACCTCTCTCAAGTGCACAG 1138
261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
1139 CAGCTCATCAAGAGCATTTAGAACCTTCAAGGCTGCCAGCTGGGGAAGACAGAGCAA 1198
281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
1199 GCCTTTGAGAACATGGACTACTTACTCTGGACTTAGACACATAGCAGAGGCTTGAGG 1258
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1259 GCATTGACTTTGGGACA 1276
321 AlaIleAspPheGlyThr 326
RESULT 12
US-10-060-634C-46
; Sequence 46, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 46
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-060-634C-46
Alignment Scores:
Pred. No.: 4.6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 15 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-060-634C-46 (1-351)
QY 299 ATGGATTATAATCTAGCTGATTCCTGATGAACGCTATGGAACCTGAGAACCTGGAAGCAG 358
DB 1 MetAspTyrLysSerGlyLeuLeuProAspGlyAsnAlaMetGluAsnLeuGluysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCTGCCCTGCCAA 418
DB 21 LeuileCysProileCysLeuGluMetPheThrLysProValValleuProCysGln 40
QY 419 CACAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTCGCAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGGTGGCTAGTGTCCATGTCTGGAGTGTGTTCCGTTGCTGCTGCTGCGCCCAT 538
DB 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGGACCGGGTGTACGCCCTGCAGAGCACTGCTGTGTGGAAC 598
DB 81 GluValIleMeAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTGTCTCCAGTCCGCCCTCCAGAAAGCGCACCCG 658
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QY 659 ATGTGGAAGGAACAGCAAGACAGAGATCAATCTACTGTCTCAGCTGTGAGTGTGCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGTCTCTTCAAGAGTGTGCGGCTCACCAGGCTGTGAGGTGCGCCCTTTGCA 778
DB 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAAGGACAGAGACTGAGCTGAGTAACTGTCATCTCCATGCTGCTGGCGGG 838
DB 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValalagly 180
QY 839 AACGACCGAGTGCAGCATCATCTCTCAGCTGAGGACTCTGTGAGAGTACCAGGAG 898
DB 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 ATATGCCACCGTGAAGGAGGCTGAGTCAAGAGTTTGACACCTCTTACCGCCATCTG 958
DB 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
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Db 61 AsnArgGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80  
QY 539 GAAGTCATCATGACCGGACCGGGGTACGGCTCAGAGGAACCTGCTGGTGAAC 598  
Db 81 GluValIleMetAspArgHisGlyValTyrglyLeuGlnArgAsnLeuValGluAsn 100  
QY 599 ATCATTGACATCTACAGCAGGAGTGTCTCCAGTCGGCCCTCGAGAAAGCAGCACCG 658  
Db 101 IleleAspIleTyrglyGlnCysSerSerArgProLeuGlnLysGlySerHisPro 120  
QY 659 ATGTGCAAGGAACACAGAGCAGAGATCAACATCTACTGTCTCAGTGTGAGTGGCT 718  
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrglyCysLeuThrCysGluValPro 140  
QY 719 ACTTGCTCTCTGCAAGGTGTGGGTCTCACCAGGCTGTGAGTGTGCCCTTGC 778  
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
QY 779 AGCATCTTCCAGGACAGAGACTGAGCTGAGTAACCTGATCTCCATGCTGTGGCGGG 838  
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGACAGATCATCTCTCAGCTGGAGGACTGTGTGAGAGTGAACGAG 898  
Db 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
QY 899 AATAGCACCATGAGTGAAGGAGCTGAGTCAGAGTTCGACACCTCTACGCCATCTG 958  
Db 201 AsnSerHisGlnValLysGluGluLeuSerHisLysPheAspAlaLeuTyrglyAla 220  
QY 959 GATGAGAAGAGCAGGAGTGTCTGACCGGATCAGCAGGAGCAGGAGGAGAGCTGG 1018  
Db 221 AspGluLysSerGluLeuGlnArgIleThrGlnGlnGlnGluLysLeuAsp 240  
QY 1019 TTCATCGAGCTGTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078  
Db 241 PheIleGluAlaLeuIleLeuGlnTyrglyArgGluGlnLeuGluLysSerThrLys 260  
QY 1079 GAGACCGCATCCAGTCCCTGGATGAGCCGGAGGGGCTACCTCTCTCAAGTGCC 1138  
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAla 280  
QY 1139 CAGCTCATCAAGACATGTAGAGGCTCCAAGGGCTGCGAGTGGGGAAGCAGAGCAA 1198  
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGlu 300  
QY 1199 GCGTTTGACAACATGAGTACTTCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGG 1258  
Db 301 GlyPheGluAsnMetAspTyrglyPheThrLeuAsnLeuGluHisIleAlaGluAla 320  
QY 1259 GCCATTGACTTTGGGACA 1276  
Db 321 AlaIleAspPheGlyThr 326

RESULT 13  
US-10-060-634C-47  
; Sequence 47, Application US/10060634C  
; Publication No. US20030219739A1  
; GENERAL INFORMATION:  
; APPLICANT: Glass, David  
; APPLICANT: Bodine, Sue  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES  
; FILE REFERENCE: REG 753A  
; CURRENT APPLICATION NUMBER: US/10/060,634C  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: 60/338,742  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/311,697  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/264,926  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: rat  
US-10-060-634C-47  
  
Alignment Scores:  
Pred. No.: 4 6e-121 Length: 351  
Score: 1671.00 Matches: 319  
Percent Similarity: 98.16% Conservative: 1  
Best Local Similarity: 97.85% Mismatches: 6  
Query Match: 58.67% Indels: 0  
DB: 15 Gaps: 0  
  
US-10-775-649-5 (1-1597) x US-10-060-634C-47 (1-351)  
QY 299 ATGGATTATTAATCTAGCTGATTCCTGATGAAACGCTATGAGAACCTGGAGAGCAG 358  
Db 1 MetAspTyrglySerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20  
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACACAGCCTGTGTCATCTGCTGCCGCCAA 418  
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
QY 419 CACAACCTCTGCCGGAAGTGTCCAACGACATCTTCCAGGCTCGCAATCCCTACTGGACC 478  
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrglyThr 60  
QY 479 AACCGGCTGGCTGAGTGTCCATGTCTGAGGTGCTTCCGTTGCCCTCGTGGCCGCAT 538  
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80  
QY 539 GAAGTCATCATGACCGGACCGGGGTACGGCTCAGAGGAACCTGCTGGTGAAC 598  
Db 81 GluValIleMetAspArgHisGlyValTyrglyLeuGlnArgAsnLeuValGluAsn 100  
QY 599 ATCATTGACATCTACAAGCAGGAGTGTCTCCAGTCGGCCCTCGAGAAAGCAGCACCG 658  
Db 101 IleleAspIleTyrglyGlnCysSerSerArgProLeuGlnLysGlySerHisPro 120  
QY 659 ATGTGCAAGGAACACAGAGCAGAGATCAACATCTACTGTCTCAGTGTGAGTGGCT 718  
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrglyCysLeuThrCysGluValPro 140  
QY 719 ACTTGCTCTCTGCAAGGTGTGGGTCTCACCAGGCTGTGAGTGTGCCCTTGC 778  
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160  
QY 779 AGCATCTTCCAGGACAGAGACTGAGTCAGTGAATCTGATCTCTCAATGCTGTGGCGGG 838  
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGACAGATCATCTCTCAGCTGGAGGACTGTGTGAGAGTGAACGAG 898  
Db 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200  
QY 899 AATAGCACCATGAGTGAAGGAGGAGTGTGAGTGTGAGAGTGTGAGAGGAGAGCTGG 958  
Db 201 AsnSerHisGlnValLysGluGluLeuSerHisLysPheAspAlaLeuTyrglyAla 220  
QY 959 GATGAGAAGAGCAGGAGTGTCTGACCGGATCAGCAGGAGCAGGAGGAGAGCTGG 1018  
Db 221 AspGluLysSerGluLeuGlnArgIleThrGlnGlnGlnGluLysLeuAsp 240  
QY 1019 TTCATCGAGCTGTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078  
Db 241 PheIleGluAlaLeuIleLeuGlnTyrglyArgGluGlnLeuGluLysSerThrLys 260  
QY 1079 GAGACCGCATCCAGTCCCTGGATGAGCCGGAGGGGCTACCTCTCTCAAGTGCC 1138  
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAla 280

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QY 1139 CAGCTCATCAAGAGCATTTGTAGAACCTCCAAAGGCGCTGCCAGCTGGGGAAGACAGAGCAA 1198
Db 281 ProLeuIleLeSerIleValGluAlaSerLysGlyCysGlnLeuGlyThrGluGln 300
QY 1199 GCGTTTGAAGACATGGACTACTTTACTCTGGACTTTAGAACACATAGCAGAGGCGCTTGGG 1258
Db 301 GlyPheGluAsnMetCysPyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 14
US-10-094-749-2861
; Sequence 2861, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2861
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2861

Alignment Scores:
Pred. No.: 1,49e-116 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-094-749-2861 (1-353)

QY 299 ATGGATTATTAATCTAGCCTGATTCCTGATGAAACGGCTATGAGAACCTGGAGAAGCAG 358
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGAGTGTTCACAGCCTGTGGTCACTCGCCCTGCCAAC 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACACCTCTCGCGGAAGTGCACACGACATCTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60
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QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTTTCCGTTGGCCCTCGTGGCGCCAT 538
Db 61 SerArgGlySerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGGACCGGCACGGGTGTACGCCCTGCAGAGGAACCTGCTGTGTGAAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTCAAGCAGGAGTGTCCAGTCCGGCCCTGCAGAAAGGACGCCACCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGAACACGAAGACGAGAGATCAACATCTACTGTCTCAGCTGTGAGTGCCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTTGTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGGTGGCCCTTTGCAA 778
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAAGGACAGAAGACTGAGCTGAGTAACTGCATCTCCATGCTGTGTGGGG 838
Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTGAGAGTGCACCAAGAG 898
Db 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgArgValThrLysGlu 200
QY 899 AATAGCCACCGAGTGAAGGAGGAGCTGAGTCAGAGTTTGACACCTCTACGCCATCTCG 958
Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAAGAGAGCGAGCTGCTGCAGCGGATCAGCGAGGAGCAGGAGAGAGCTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSer 240
QY 1019 TTCATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleGlnGlnTyrGlnGluGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGCCATCCAGTCCCTCGATGAGCCCGGAGGGGTACCTCTCTCAAGTGCCAA 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTTGTAGAAGCCTCCAAGGCTGCCAGCTGGGGAAGACAGAGCAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGAACATGGACTACTTTACTCTGAGCTTAGAACACATAGCAGAGGCGCTTGGG 1258
Db 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 15
US-10-221-625-85
; Sequence 85, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILIMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
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/ APPLICANT: AU-YOUNG, Janice
/ APPLICANT: REDDY, Roopa
/ TITLE OF INVENTION: TRANSCRIPTION FACTORS
/ FILE REFERENCE: PF-0761 PCT
/ CURRENT APPLICATION NUMBER: US/10/221,625
/ CURRENT FILING DATE: 2001-03-13
/ NUMBER OF SEQ ID NOS: 214
/ SOFTWARE: PERL Program
/ SEQ ID NO 85
/ LENGTH: 353
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20040033942A1 3575519CD1
US-10-221-625-85

Alignment Scores:
Pred. No.: 1.49e-116 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-221-625-85 (1-353)

QY 299 ATGGATTATTAATCTAGCTGATCTCTGATGGAAACGCTATGAGAACCTGGAGACG 358
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20

QY 359 CTGATCTGCCCATCTCCCTGGAGATGTTTACCAAGCCTGTGTCTCATCTCGCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40

QY 419 CACAACCTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTCGCAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60

QY 479 AACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCGCCCTCGCGCCCAT 538
Db 61 SerArgLysSerSerValSerMetSerGlyLysArgPheArgCysProThrCysArgHis 80

QY 539 GAAGTGATCATGGACCGGACGGGGTGTACGGCCTGCAGAGGAACCTGTGTGGAAAAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100

QY 599 ATCATTGACATCTACAAGCAGGAGTGCTCCAGTGGCCCTCGCAGAAAGCGACCCCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120

QY 659 ATGTGCAAGGAAACACGACGAGAGATCAACATCTACTGTCTCACGTTGAGGTGCCT 718
Db 121 MetCysLysGlnHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140

QY 719 ACTTGCTCTTGTGCAAGTGTGTTGGGGCTCACCGCCTGTGAGGTTGCCCTTTGCCAA 778
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160

QY 779 AGATCTTCCAAAGGACAGAAGACTGAGCTGAGTACTGCATCTCCATGCTGTGTGGCGGG 838
Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180

QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGACCCAGGAG 898
Db 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGlu 200

QY 899 AATAGCCACCGAGTGAAGGAGGAGTGTAGTCAAGTTTGCACACCTCTACGCCCATCTGT 958
Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220

QY 959 GATGAGAAGAACGCGAGCTGTCTGACCGGATCAACGACGAGGAGGAGGAGCTGGGC 1018
Db 959 GATGAGAAGAACGCGAGCTGTCTGACCGGATCAACGACGAGGAGGAGGAGCTGGGC 1018

221 AspGluLysLysSerGluLeuGlnArgIleThrGlnGluGlnGluLysLysLeuSer 240
1019 TTCATCGAGGCTCTGATCTCCAGTACACGGGAGCAGCTGGAAAGTCCACCAAGCTTGTG 1078
241 PheIleGluAlaLeuIleGlnGlnTyrGlnGlnGlnLeuAspLysSerThrLysLeuVal 260
1079 GAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCACAAG 1138
261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
1139 CAGCTCATCAAGACGATTTAGAACCTCCAAAGGGTGCAGCTGGGGAGACAGACGAA 1198
281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
1199 GCCTTTGAGAACATGCACTACTTCTCTGGAATTAGAACACATACAGACGAGCCTTGAGG 1258
301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
1259 GCCATTGACTTTGGGACA 1276
321 AlaIleAspPheGlyThr 326

RESULT 16
US-09-764-864-808
; Sequence 808, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 808
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-808

Alignment Scores:
Pred. No.: 1.65e-116 Length: 366
Score: 1612.50 Matches: 308
Percent Similarity: 94.19% Conservative: 16
Best Local Similarity: 89.53% Mismatches: 15
Query Match: 56.62% Indels: 5
DB: 9 Gaps: 1

US-10-775-649-5 (1-1597) x US-09-764-864-808 (1-366)

QY 245 AGACAAGACTTGTGTGTGACGCGAGGTGGGCAAGACAGTGCATTTCAAAGCAATATGGAT 304
Db 1 ArgArgGlnLeuGlyValAlaLeuIlePro-----SerHisArgMetAsp 15

QY 305 TATAATCTAGCTCATCTCTGATGAAACGCTATGAGAACTGAGAGAACCTGAGAGAGCAGCTGATC 364
Db 16 TyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGlnLeuIle 35

QY 365 TCCTCCATCTGCTGGAGATGTTTACCAAGCTGTGGTTCATCTGCGCTTGCACCAACAAC 424
Db 36 CysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGlnHisAsn 55

QY 425 CTCTCCCGGAGTGTGCCAACGACATCTCCAGGCTGGAGTCCCTCTCTGCGCCCATGAAGTG 484
Db 56 LeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThrSerArg 75

QY 485 GGTGGCTCAGTCTCCATGTCTGAGTCTGTTTCCGTTGCGCTCTGCTGCGCCCATGAAGTG 544
Db 76 GlySerSerValSerMetSerGlyArgPheArgCysProThrCysArgHisGluVal 95

QY 545 ATCATGGACCGGACGCGGGTGTACGGCTGACAGGAACCTGCTGGTGGAAACATCATTT 604
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Db 96 IleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleIle 115  
QY 605 GACATCTACAACGAGGAGTCTCCAGTCGGCCCTCGCAGAAAGCGACCCACCGCATGTGC 664  
Db 116 AspIleTyrLysGlnGluCysSerArgProLeuGlnLysGlySerHisProMetCys 135  
QY 665 AAGGACACGAGACGAGAGAGATCAACATCTACTGTCTCAGTCGTGAGGTGCTTCTGCG 724  
Db 136 LysGluHisGluAspGluLysAsnIleTyrCysLeuThrCysGluValProThrCys 155  
QY 725 TCCTTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGTCCTTGTCAAGCATC 784  
Db 156 SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal 175  
QY 785 TTCCAAGGACAGAGACGAGTGAAGTAACTCACTCTCCATCTCGTGTGCGGGGAAACGAC 844  
Db 176 PheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGlyAsnAsp 195  
QY 845 CGAGTGCAGACCATCTCTCAGCTGAGGAGTCTGTGAGAGTGCACCGAGAGATAGC 904  
Db 196 ArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGluAsnSer 215  
QY 905 CACCAAGTGAAGGAGGAGTGAAGTGAAGTTTGACCCCTCTACGCCATCTCGGTGAG 964  
Db 216 HisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeuAspGlu 235  
QY 965 AAGAAAGAGCGAGCTGTGAGCGGATCACGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 1024  
Db 236 LysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnLysLysLeuSerPheIle 255  
QY 1025 GAGGCTCTGATCTCTCAGTACAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1084  
Db 256 GluAlaLeuIleGlnTyrGlnGlnLeuAspLysSerThrLysLeuValGluThr 275  
QY 1085 GCCATCCAGTCTCTGAGTGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1144  
Db 276 AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLysGlnLeu 295  
QY 1145 ATCAAGAGCATTTGTAAGCCCTCAAGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTT 1204  
Db 296 IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGlnGlnPhe 315  
QY 1205 GAGACATGAGTACTTTACTCTGAGTCTAGAACATAGACAGAGCCCTTGAGGCCATT 1264  
Db 316 GluAsnMetAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle 335  
QY 1265 GACTTTGGGACA 1276  
Db 336 AspPheGlyThr 339

RESULT 17  
US-10-061-043A-48  
; Sequence 48, Application US/10061043A  
; Publication No. US20030129686A1  
; GENERAL INFORMATION:  
; APPLICANT: Glass, David  
; APPLICANT: Bodine, Sue  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES  
; FILE REFERENCE: REG 753B  
; CURRENT APPLICATION NUMBER: US/10/061, 043A  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: 60/338, 742  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/311, 697  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/264, 926  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 353  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-061-043A-48  
Alignment Scores:  
Pred. No.: 1,786-116 Length: 353  
Score: 1612.00 Matches: 305  
Percent Similarity: 97.24% Conservative: 12  
Best Local Similarity: 93.56% Mismatches: 9  
Query Match: 56.60% Indels: 0  
DB: 14 Gaps: 0  
US-10-775-649-5 (1-1597) x US-10-061-043A-48 (1-353)  
QY 299 ATGGATTATAATCTAGGCTGATTCCTGATGAAACGCTATGAGAACCTGAGAAAGCAG 358  
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20  
QY 359 CTGATCTCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCATCTGCTGCCCTGCCAA 418  
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40  
QY 419 CACAACCTCTGCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC 478  
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60  
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCTGTTCCGTTGCCCTCGTCCGCCAT 538  
Db 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80  
QY 539 GAAGTGATCATGACCGGACGCGGTGTACCGCCTGCAGAGGAACCTGCTGCTGGAACAC 598  
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100  
QY 599 ATCATTGATCATCTACAAGCAGGAGTCTCCAGTCCGCGCCCTGCAGAAAGCGACCCCG 658  
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120  
QY 659 ATGTCAAGAGAACAGAGACGAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCT 718  
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140  
QY 719 ACTTGCTCTCTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCTGCCCTTTGCAA 778  
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160  
QY 779 AGCATCTTCCAAGGACAGAAAGTCAAGTCACTGATGATTAATCTCCATCTGCTGTGCGGG 838  
Db 161 SerValPheGlnGlyLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180  
QY 839 AACGACCGAGTGCAGACCATCTCTCAGCTGGAGGACTCTGTGAGAGTGCACCAAGGAG 898  
Db 181 AsnAspArgValGlnThrIleTyrThrGlnLeuGluAspSerArgArgValThrLysGlu 200  
QY 899 AATAGCCACCGAGTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 958  
Db 201 AsnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220  
QY 959 GATGAGAAAGAGAGCGAGTCTGCGAGCGGATCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1018  
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuSer 240  
QY 1019 TTCACTCGAGGTCTCTGATCTCTCAGTACAGGAGGAGTGAAGTGAAGTGAAGTGAAG 1078  
Db 241 PheIleGluAlaLeuIleGlnTyrGlnGlnLeuAspLysSerThrLysLeuVal 260  
QY 1079 GAGACCGCATCCAGTCTCTGATGAGCGCGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1138  
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280  
QY 1139 CAGCTCATCAAGAGCATTTGTAGAAGCTTCCAAGGCTGCAGCTGGGGAAGACAGAGCAA 1198  
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300  
QY 1199 GCCTTTGAGAACATGAGTACTTTTACTCTGGACTTAGAACACATAGACAGAGCCCTTGAGG 1258

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Db 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 18
US-10-060-634C-48
; Sequence 48, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-634C-48

Alignment Scores:
Pred. No.: 1.78e-116 Length: 353
Score: 1612.00 Matches: 305
Percent Similarity: 97.24% Conservative: 12
Best Local Similarity: 93.56% Mismatches: 9
Query Match: 56.60% Indels: 0
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-060-634C-48 (1-353)
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QY 359 CTGATCTGCCCATCTGCTCGGAGATGTTTACCAAGCCTGTGTCTATCTGCGCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTCTGCGGGAAGTGTGCCAACGACATCTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTGCTTCCGTTGCCCTCGTCCGCCCAT 538
Db 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTATCATGGACCGGACGGGTGTACGGCTCAGAGGACCTGCTGTGGTGGAAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGAGTGTCTCAGTCGGCCCTCGAGAAAGCAGCACCGG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGAACACGAAGACGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGGTGCCCTTTGCA 778
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
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QY 779 AGCATCTTCCAAGGACAGAGACTGAGCTGAGTAACATGCATCTCCATCTGCTGGTGGCGGG 838
Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGACTCGTGCAGAGTAGACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleTyrThrGlnLeuGluAspSerArgValThrLysGlu 200
QY 899 AATAGCCACAGGTGAAGGAGGAGCTGAGTCAGAGTTTGCACACCTCTACGCCATCCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGAAGCGAGCTGCTGCAGCGGATCACGACGAGGACGAGAGAGCTGGGC 1018
Db 221 AspGluLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuSer 240
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGGAGCTGGAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleGlnGlnTyrGlnGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATTCAGTCCCTCGATGATGAGCCGCGGAGGGGCTACCTCTCTCAAGTGCAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTCGTAGAAGCCTCCAAAGGCTGCAGCTGGGGGAGACAGAGCAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGAGTACTTTACTCTGGACTTAGAACACATACGAGCGCTTGAGG 1258
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QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 19
US-10-204-921-57
; Sequence 57, Application US/10204921
; Publication No. US20050095567A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purvi
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
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Db      61 ArgCysProThrCysArgHisGluValIleMetAspArgHisGlyValTyrGlyLeuGln 80
QY      578 AGAACCTCTGCTGGTGAATAACATCATATGACATCTACAAGCAGAGTGTCCAGTGGGCC 637
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QY      638 CTGCAGAAAGGAGCCACCGATGTCAAGGACACGAGACGAGAGATCAACATCTAC 697
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QY      698 TGTCTCACGTGTGAGTGCCTACTTGTCTCTTGTGCAAGGTGTTGGGGCTCACCAGGCC 757
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Db      141 CysGluValAlaProLeuGlnSerValPheGlnGlyGlnLysThrGluLeuAsnAsnCys 160
QY      818 ATCTCCATCTGTCGTGGCGGGAACGACCGAGTGCAGACCATCATCTCTCAGCTGGAGGAC 877
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QY      878 TCGTCAGAGTGCACCAAGGAGAAATAGCCACCAAGGTGAAGGAGGAGCTGAGTCAGAAGTTT 937
Db      181 SerArgArgValThrLysGluAsnSerHisGlnValLysGluLeuSerGlnLysPhe 200
QY      938 GACACCTCTACGCCATCTCGATGAGAGAGAGAGAGAGAGAGCTGTCAGCGGATCAGCGAG 997
Db      201 AspThrLeuTyrAlaIleLeuAspGluLysLysSerGluLeuGlnArgIleThrGln 220
QY      998 GAGCAGGAGGAGAGCTGGGCTTCATCGAGGCTCTGATCCTCCAGTACAGGGAGCAGCTG 1057
Db      221 GluGlnGluLysLeuSerPheIleGluAlaLeuIleGlnTyrGlnGluGlnLeu 240
QY      1058 GAAAGTCCACCAAGCTTGTGGAGACCGCATCCAGTCCCTGGATGAGCCCGAGGGGCT 1117
Db      241 AspLysSerThrLysLeuValGluThrAlaIleGlnSerLeuAspGluProGlyGlyAla 260
QY      1118 ACCTTCCTCTCAAGTCCCAAGCAGCTCATCAGAGCATTTAGAGCCTCCAGGGCTGC 1177
Db      261 ThrPheLeuLeuThrAlaLysGlnLeuIleLysSerIleValGluAlaSerLysGlyCys 280
QY      1178 CAGCTGGGAACAGACAGCAAGCTTTGAGAACATGGACTTCTTACTCTGGACTTAGAA 1237
Db      281 GlnLeuGlyLysThrGluGlnGlyPheGluAsnMetAspPhePheThrLeuAspLeuGlu 300
QY      1238 CACATAGCAGGCTTGGGGCCATTGACTTTGGGACA 1276
Db      301 HisIleAlaAspAlaLeuArgAlaIleAspPheGlyThr 313

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Search completed: June 15, 2005, 15:09:10  
Job time : 144 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:10:59 ; Search time 840 Seconds  
(without alignments)  
11254.556 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597

Sequence: 1 ctcgagattacccttacag.....Gaaataaattatctgtgcc 1597

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1597	100.0	1597	6	ABA99063 Murine mu
2	890.8	55.8	1053	6	Abq79506 Rat MURF1
3	803.8	50.3	2097	6	Abq79507 Human MUR
4	802.2	50.2	1231	5	Aah90037 Human bon
5	802.2	50.2	1764	5	Abag3058 Human tra
6	802.2	50.2	2700	12	Adq24981 Human sof
7	800.6	50.1	1764	10	Ada53654 Human cod
8	797.4	49.9	1781	4	AAS25842 Human cdn
9	797.4	49.9	1781	8	Abx73183 Human nov
10	747.8	46.8	1757	6	Abx70380 Human bon
11	747.8	46.8	2110	5	Aas42490 Human cdn
12	679.8	42.6	1796	5	Aah89924 Human bon
13	674	42.2	1183	5	Aah90117 Human bon
14	547.4	34.3	630	6	Abq79510 Rat MURF1
15	484.6	30.3	1431	6	ABA99061 Murine mu
16	481.8	30.2	1405	10	ADC30183 Human nov
17	481.8	30.2	1913	5	Aah68563 Human pro
18	481.8	30.2	1390	4	Aah78026 Nucleotid
19	480.2	30.1	1349	3	Aaa72433 Human nuc
20	444.4	27.8	867	6	Abq79512 Human MUR

21	432.2	27.1	2590	6	ABA99062	Abag99062 Murine mu
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23	430.6	27.0	2434	8	AAD49597	Aad49597 Human cyt
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25	430.6	27.0	2662	12	ADQ24315	Adq24315 Human sof
26	421.2	26.4	1762	4	AAS25855	Aas25855 Human cdn
27	421.2	26.4	1762	8	ABX73196	Abx73196 Human nov
28	412.2	25.8	1426	10	ADC30799	Adc30799 Human nov
29	390	24.4	531	3	AAC75285	Aac75285 Human ORF
30	390	24.4	531	6	ABN78104	Abn78104 Human int
31	374.2	23.4	1500	4	AAF27653	Aaf27653 DNA encod
32	329.4	20.6	2040	6	ABN85313	Abn85313 Human cyt
33	277	17.3	1039	6	AAD42866	Aad42866 Human DNA
34	277	17.3	1039	10	ADH62597	Adh62597 Human ven
35	260.6	16.3	424	9	ACH18104	Ach18104 Human adu
36	246.4	15.4	411	9	ACH17597	Ach17597 Human adu
37	244.2	15.3	446	4	AAS26303	Aas26303 Human cdn
38	244.2	15.3	446	8	ABX73644	Abx73644 Human nov
39	220.6	13.8	2762	12	ADP22641	Adp22641 Sea-squir
40	218.8	13.7	573	10	ADC32553	Adc32553 Human nov
41	217.8	13.6	587	4	AAS26314	Aas26314 Human cdn
42	217.8	13.6	587	8	ABX73655	Abx73655 Human nov
43	141.6	8.9	766	12	ADQ25137	Adq25137 Human sof
44	141.6	8.9	2000	11	ACN89140	Actn89140 Breast ca
45	123.4	7.7	475	12	ADQ21255	Adq21255 Human sof

ALIGNMENTS

RESULT 1

ABA99063  
ID ABA99063 standard; DNA; 1597 BP.

XX ABA99063;

DT 15-JUL-2002 (first entry)

DE Murine muscle ring finger protein 3 (MURF-3) coding sequence.

KW Muscle ring finger; MURF-3; mouse; cardiant; microtubule;

KW intermediate filament; striated muscle; cardiac hypertrophy;

KW heart disease; gene; db.

OS Mus musculus.

EH Key Location/Qualifiers

FT CDS 299..1330

FT /\*tag= a

FT /product= "MURF-3"

XX WO200206318-A2.

XX PD 24-JAN-2002.

XX PF 18-JUL-2001; 2001WO-US022896.

XX PR 18-JUL-2000; 2000US-0219020P.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX OL Olson EN, Spencer JA;

XX DR WPI; 2002-241506/29.

XX P-P SDB; ABB08277.

PT Novel muscle ring finger protein useful for drug screening, and for  
diagnosing and treating diseases, particularly cardiomyopathies.

XX Claim 4; Page 131-133; 134pp; English.

XX The sequence encodes murine muscle ring finger protein 3 (MURF-3). The  
invention relates to a purified muscle ring finger (MURF) protein,

CC selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the  
CC invention are involved in microtubule and intermediate filament  
CC stabilization of striated muscle cells and have cardiac activity. The  
CC MURF proteins are useful for screening a candidate substance for MURF  
CC protein-binding activity, in a cell, cell-free system or in vivo, and its  
CC effect on interaction of MURF with microtubules, homodimerisation of  
CC MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction  
CC of MURF with intermediate filaments, e.g. desmin, vimentin and  
CC cyokeratin, and heterodimerisation of MURF. The screened compounds are  
CC useful for treating and preventing cardiac hypertrophy and heart  
CC diseases. MURF proteins are useful as antigens to immunise animals for  
CC the production of antibodies  
XX  
SQ Sequence 1597 BP; 405 A; 404 C; 438 G; 350 T; 0 U; 0 Other;

Query Match 100.0%; Score 1597; DB 6; Length 1597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTCGAGATTACCCCTTACAGAACTGTTCGGAGCACCTTTCCCTTGGCAGCACACTCAG 60

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DB 121 GCAGACCATGGATAACTTGGAAAGCACTGATCTGCCATCTGCTTCCATCTGCTTAC 180

QY 181 GAAGCTGTGGTCACTTCTCCCTTGCAGACCACTGTGCAGAAATGTGCGGGCCCCC 240  
DB 181 GAAGCTGTGGTCACTTCTCCCTTGCAGACCACTGTGCAGAAATGTGCGGGCCCCC 240

QY 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGCAAGACAGTGCATTTCAAAGCAATAT 300  
DB 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGCAAGACAGTGCATTTCAAAGCAATAT 300

QY 301 GGATTATAATCTAGCCTGATCTGTATGGAAACGCTATGGAAACCTGGAGAACGAGCT 360  
DB 301 GGATTATAATCTAGCCTGATCTGTATGGAAACGCTATGGAAACCTGGAGAACGAGCT 360

QY 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCTGTGCTCATCTGCCCTGCCAACA 420  
DB 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCTGTGCTCATCTGCCCTGCCAACA 420

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DB 421 CAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480

QY 481 CCGGGTGGCTCAGTGTCCATGCTCGAGGTGCTTTCCGTTGGCCCTCGTCCGCCATGA 540  
DB 481 CCGGGTGGCTCAGTGTCCATGCTCGAGGTGCTTTCCGTTGGCCCTCGTCCGCCATGA 540

QY 541 AGTGATCATGGACCGGCGGTGTACGGCTGTGAGGAACTGCTGGTGGAAACAT 600  
DB 541 AGTGATCATGGACCGGCGGTGTACGGCTGTGAGGAACTGCTGGTGGAAACAT 600

QY 601 CATTGACATCTAAGCAGGAGTGTCTCCAGTCCGGCCCTGCAGAAAGGCGCACCCGAT 660  
DB 601 CATTGACATCTAAGCAGGAGTGTCTCCAGTCCGGCCCTGCAGAAAGGCGCACCCGAT 660

QY 661 GTGCAAGGACACGAGAGAGAGATCAACATCTACTGCTCAGCTGTGAGGTGCTTAC 720  
DB 661 GTGCAAGGACACGAGAGAGAGATCAACATCTACTGCTCAGCTGTGAGGTGCTTAC 720

QY 721 TTGCTCTTGTGCAAGGTGTTTGGGGCTCACAGGCTGTGAGGTGCTTGGCAAG 780  
DB 721 TTGCTCTTGTGCAAGGTGTTTGGGGCTCACAGGCTGTGAGGTGCTTGGCAAG 780

QY 781 CATCTTCCAAAGACAGAGACTGAGTGAATCTGATCTCCATCTGCTGGTGGGGGAA 840  
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DB 781 CATCTTCCAAAGACAGAGACTGAGTGAATCTGATCTCCATCTGCTGGTGGGGGAA 840  
QY 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTCAGAGTGCACCAAGAGAA 900  
DB 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTCAGAGTGCACCAAGAGAA 900  
QY 901 TAGCCACCAAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCTCTGGA 960  
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DB 1021 CATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTGGGAAAGTCCACCAAGTCTTGGGA 1080  
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QY 1141 GCTCATCAAGAGCATTTGTAAGCCCTCAAGGGCTGCCAGCTGGGAGACAGAGCAAG 1200  
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QY 1201 CTTTGAGACATGGACTACTTTTACTCTGACCTTAGAACACATAGCAGAGCCCTTGAGGGC 1260  
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DB 1381 AGGTCTCTTATGGAGCCCTGACTGCTTAGTAGTGTCTTAAGTAGACCAAGCTGCTCG 1440  
QY 1441 AACACATAGAGATCTATCTTGGCCATCTCTGCTTTTGAGGGATGAGATAAAGGCAATGT 1500  
DB 1441 AACACATAGAGATCTATCTTGGCCATCTCTGCTTTTGAGGGATGAGATAAAGGCAATGT 1500  
QY 1501 GCCCACCATGCTGGCTCCACAGACAACTTTGTGATGATGCCAGGTCTGGGACAGTGCC 1560  
DB 1501 GCCCACCATGCTGGCTCCACAGACAACTTTGTGATGATGCCAGGTCTGGGACAGTGCC 1560  
QY 1561 TGGTACATAATTTGTTTCGAAATAAATTAATCTCGTGCC 1597  
DB 1561 TGGTACATAATTTGTTTCGAAATAAATTAATCTCGTGCC 1597

RESULT 2  
ABQ79506  
ID ABQ79506 standard; DNA; 1053 BP.  
XX  
AC ABQ79506;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Rat MURF1 protein encoding DNA.  
XX  
KW Muscle atrophy protein; MURF1; MURF3; MAFB3; atrophy; neuroprotective;  
XX gene therapy; transgenic; gene; rat; ds.  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1053  
FT /\*tag= a



PA	(REGE-)	REGENERON PHARM INC.
XX	Glass DJ,	Bodine SC;
PI	WPI;	2002-608513/65.
XX	P-PSDB;	ABB81135.
DR	Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g. MURF1, MURF3 or MAFBX, useful for treating muscle atrophy and other related disorders, e.g. Guillian-Barre syndrome, peripheral neuropathy, PT and nerve damage.	
PT	Claim 2; Fig 8A-C; 104pp; English.	
XX	The invention relates to isolated nucleic acid molecules encoding muscle atrophy proteins MURF1, MURF3, or MAFBX. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and polypeptides are useful for treating muscle atrophy or detecting atrophy, CC and for treating related diseases/disorders, e.g. Guillian-Barre syndrome, peripheral neuropathy, or nerve damage caused by environmental CC toxins or drugs. The MURF1, MURF3 and MAFBX antagonists, and the CC antagonists of their pathways are useful for inhibiting atrophy, inducing CC hypertrophy, decreasing ubiquitination, interfering with the ubiquitin CC pathway, or modulating MURF1, MURF3 or MAFBX expression or activity. The CC nucleotide sequences are useful for diagnostic and genetic testing. The CC present sequence represents a human MURF1 protein encoding DNA	
XX	Sequence 2097 BP; 565 A; 460 C; 604 G; 468 T; 0 U; 0 Other;	
SQ	Query Match 50.3%; Score 803.8; DB 6; Length 2097; Best Local Similarity 86.2%; Pred. No. 1.1e-203; Matches 889; Conservative 0; Mismatches 142; Indels 0; Gaps 0;	
QY	262	GAGCGAGTGGGCAAGACAGCTGCATTTCAAGCAATATGGATTATAATCTAGCCGTAT 321
DB	399	GAGGCGAGCTAGGCGTGGCTCTCATCTTCCCAAGAAATGGATTATAAGTCGAGCCGTAT 458
QY	322	TCTGTATGAAACCGCTATGAGAACCTGGAGAGCAGCTGATCGCCCATCTGCCTGGA 381
DB	459	CCAGGATGGGATCCCATGAGNACTTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGGA 518
QY	382	GATGTTTACCAAGCCTGTGGTATCTGCTGCCCTGCCAACAACCTCTGCCGGAAGTGTC 441
DB	519	GATGTTTACCAAGCAGTGGTATCTTGGCTGCCAGCACAACCTGTGCCGGAAGTGTC 578
QY	442	CAAGCATCTTCCAGGCTGCGNATCCCTACTGGACCAACCGGCTGCTCAGTGCCAT 501
DB	579	CAATGACATCTTCCAGGCTGCAATCCCTACTGGACCAACCGGCGAGCTCAGTGCCAT 638
QY	502	GTCTGGAGGTGCTTTCCGTTGCCCTCGTGCCGCCATGAAGTGATCATGGACCGGACGG 561
DB	639	GTCTGGAGGCCGTTTCGGCTGCCACCTGCCGCCACGAGGTGATCATGGATCGTCACGG 698
QY	562	GGTGTAACGGCTGCAGAGAACTGTGTGTGGAATAACATCATTTGACATCTACAGCAGGA 621
DB	699	AGTGTAACGGCTGCAGAGAACTGTGTGTGGAATAACATCATTCATCAAAACAGGA 758
QY	622	GTGCTCCAGTCCGCCCTCGAAGAGGAGCCAGCCAGTGTGCAAGGACACGAGACCA 681
DB	759	GTGCTCCAGTCCGCCCTCGAAGAGGAGTCAACCCATGTGCAAGGACACGAGATGA 818
QY	682	GAAAGTCAACATCTACTGTCTCACGTGTGAGGTGCCCTACTTGTCTCTGCAAGGTGTT 741
DB	819	GAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCTACTTGTCTCTGCAAGGTGTT 878
QY	742	TGGGGCTCACCGAGCCTGTGAGGTGCCCTTTGCAAGATCTTCCAAAGGACAGAAAGAC 801
DB	879	TGGGATCCCAAGGCCCTGCGAGGTGCCCTTTCAGAGAGTGTCTTCAGGACAAAAGAC 938
QY	802	TCAGCTGAGTAAGTATCTCCATGCTGGTGGGGGACGACCGGATCGACGATCAT 861
DB	939	TGAACCTGAATACTGTATCTCCATGCTGGTGGGGGGAATGACCCGTGTGCAGACCATCAT 998
QY	862	CTCTCAGCTGGAGGACTCGTCAGAGTACCACAGAGAGATAGCCACGAGTGAGGAGGA 921
DB	999	CACCTAGCTGGAGGATTCCTCGTGCAGTGACCAAGGAGAACAGTCCACAGGTAAAGGAGA 1058
QY	922	GCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTCTGGATGAGAAAGAGCGAGTGTCT 981
DB	1059	GCTGAGCCAGAAAGTTTGACACCGTTGTATGCCATCTCTGGATGAGAAAGAGTGTGTCT 1118
QY	982	GCAGCGGATCAGCAGGAGCAGGAGGAGCTGGCTTTCATCGAGGCTCTGATCTCTCA 1041
DB	1119	GCAGCGGATCAGCAGGAGCAGGAGGAGGAAAGTTTACCTTCATCGAGGCCCTCATCCAGCA 1178
QY	1042	GTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTTGGGAGACCGCCATCCAGTCCCTCGA 1101
DB	1179	GTACAGGAGCAGCTGGACAGTCCACAAAGCTGGTGGAACTGCGCATCCAGTCCCTCGA 1238
QY	1102	TGAGCCCGGAGGGGTACCTTCTTCAAGTGCCCAAGCAGCTCATCAAGAGCATTTGAGA 1161
DB	1239	CGAGCTGGGGGAGCCACCCTTCTTGACTGCCAAGCAACTCATCAAAAGCATTTGTGGA 1298
QY	1162	AGCTCCAGGCGTCCAGCTGGGGAAGACAGCAAGCGCTTTGAGAACATGGACTACTT 1221
DB	1299	AGCTTCCAAAGGCTGCCAGCTGGGGAAGACAGCAGAGGGCTTTGAGAACATGGACTTCT 1358
QY	1222	TACTCTGGACTTTAGAACACATAGCAGAGCGCTTGAGGGCCATTGACTTTGGGACAGGTA 1281
DB	1359	TACTTTGGATTTAGACCATAGCAGACGCCCTTGAGAGCCATTGACTTTGGGACAGATGA 1418
QY	1282	AGGATGTGATG 1292
DB	1419	GGAAGAGGAAG 1429
RESULT 4		
AAH90037		
ID	AAH90037 standard; cDNA; 1231 BP.	
XX	AAH90037;	
XX	01-OCT-2001 (first entry)	
XX	Human bone marrow cDNA, SEQ ID NO: 281.	
XX	Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antitviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.	
OS	Homo sapiens.	
XX	WO200153453-A2.	
PN	26-JUL-2001.	
XX	23-DEC-2000; 2000WO-US034960.	
XX	23-DEC-1999; 99US-00471275.	
PR	21-JAN-2000; 2000US-00488725.	
PR	25-APR-2000; 2000US-00552317.	
PR	20-JUN-2000; 2000US-00598042.	
PR	19-JUL-2000; 2000US-00620312.	
PR	03-AUG-2000; 2000US-00653450.	
PR	14-SEP-2000; 2000US-00662191.	
PR	19-OCT-2000; 2000US-00693036.	
PR	30-NOV-2000; 2000US-0250583P.	
XX	(HYSE-) HYSEQ INC.	
XX	Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;	
PI	Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;	
PI	Zhou P, Drmanac RT;	
XX		







D	b		992	GAGCGACGTAGGCGTGGCTCTCATTCCTTCCCA CAGAATGAATTATTAAGTCGACGCCTGAT	1051
Q	y		322	TCCTGATGGAAACGCTATGGAGAACCTGGAGAACGAGCTGATCTGCCCCCATCTGCCTCGGA	381
D	b		1052	CCAGGATGGGAATCCCATGGAGAACTTGGAGAACGAGCTGATCTGCCCTATCTGCCTTGGA	1111
Q	y		382	GATGTTTACCAGGCTGTGFTCATCTTGCCTCTGCCAACAACCTCTGCCGGAAGTGTCG	441
D	b		1112	GATGTTTACCAGCGACGTGGTGCATCTTGGCCTGCGACACAACCTGTGTCGGAAGTGTCG	1171
Q	y		442	CAACGACATCTTCCAGGCTCGAATCCCTACTGTGACCAACCGCGGTGCGCTCAGTGTCAT	501
D	b		1172	CAATGACATCTTCCAGGCTCGAATCCCTACTGTGACCAACCGCGGTGCGCTCAGTGTCAT	1231
Q	y		502	GTCTGGAGGTGCTTTCCTGTTGCCCTCGTGC CGCCATGAAGTGATCATGGACCGGCACGG	561
D	b		1232	GTCTGGAGGCGTTCCTGCTGCCCACTTGC CGCCACGAGGTGATCATGGATCGTCACGG	1291
Q	y		562	GGTGTA CGGCTCGCAGAGGAACCTGCTGGTGGGAAAA CATATTGACATCTACAAGCAGGA	621
D	b		1292	AGTGTA CGGCTCGCAGAGGAACCTGCTGGTGGGAAAA CATCATCGACATCTACAAA CAGGA	1351
Q	y		622	GTGCTCCAGTCGGCCCCCTGCAGAAAGCAGCCACCGATGTGCAAGNAACACGNAGACGA	681
D	b		1352	GTGCTCCAGTCGGCCCCCTGCAGAAAGGCGAGCTCACCCATGTGCAAGGAGCAGCAAGAATGA	1411
Q	y		682	GAAGATCAA CATCTACTGTCTCAGCTGTAGGTGCTTACTTGGCTCTTGTGCAAGGTGTT	741
D	b		1412	GAATAATCAA CATCTACTGTCTCAGCTGTAGGTGCTTACTTGGCTCTTGTGCAAGGTGTT	1471
Q	y		742	TGGGGCTCA CACAGGCTGTGAGGTGGCCCCCTTTGCA AAGCATCTTCCAAGSACAGAA GAC	801
D	b		1472	TGGGATCCACAAGGCTTCGAGGTGGCCCCCATTCGAGAGTGTCTTCAGGSA CAAAA GAC	1531
Q	y		802	TGAGCTGAGTAACTGCA TCTCCATCTGTGTGGCGGGGAA CGACCGAGTGCNAGCATCAT	861
D	b		1532	TGAATGAATAACTGTATCTCATCTGTGTGGCGGGGAA TGACCGTGTGCAGACCATCAT	1591
Q	y		862	CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAA TAGCCACACAGGTGAAGGAGGA	921
D	b		1592	CACCTCAGCTGGAGATTTCCCGTCAGGTGACCAAGAGNA CAGTCCACAGGTAAAGGAAGA	1651
Q	y		922	GCTGAGTCAGAA GTTGA CACCTCTACGCCATCTTGATGAGAAAGACGAGCTGCT	981
D	b		1652	GCTGAGCCAGA AGTTTGACACGTTGTATGCCATCTCTGATGAGAAAGAAAGTGAGTTGCT	1711
Q	y		982	GCAGCGGATCACG CAGAGCAGGAGGAGAGCTGGGCTTCATTCAGAGCTCTGATCTCTCCA	1041
D	b		1712	GCAGCGGATCACG CAGGAGCAGGAGAAAAGCTTAGCTTCA TCAGAGCCCTCATPCCA GCA	1771
Q	y		1042	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGAGACCGCCCATCCAGTCCCTCGGA	1101
D	b		1772	GTAC CAGAGCAGCTGGACAAGTCCAAAGCTGGTGGAA ACTGCCATCCAGTCCCTCGGA	1831
Q	y		1102	TGAGCCCGGAGGGGCTACTTCTCTCAAGTGCCAAGCAGCTCATCAAGAGCATTTGTAGA	1161
D	b		1832	CGAGCTTGGGGAGCGACCTTCTCTTGACTGCCAAGCAACTCATCAAAGCATTTGTGGA	1891
Q	y		1162	AGCTTCCAGGGGCTCGCAGCTGGGGGAGACAGAGCAAGGCTTTGAGAACATGCACTACTT	1221
D	b		1892	AGCTTCCAGGGGCTGCCAGCTGGGGGAGACAGAGCAGGGCTTTTGAGAACATGCACTACTT	1951
Q	y		1222	TACTCTGGACTTAGNA CACATAGCAGAGGGCTTCAGGGGCCATTACATTTGGGACAGGTAA	1281
D	b		1952	TACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGGCCATTGACTTTGGGACAGATGA	2011
Q	y		1282	AGGATGTGATG	1292
D	b		2012	GGAAGAGGAAG	2022
RESULT 7 ADAS3654					

Db 400 AGTTTACGGCCTCGACAGGAACCTGCTGTGGAGAACATCATCGACATCTACAAAACGGA 459  
QY 622 GTGCTCCAGTCGGCCCTCGAGAAAGCGACGCCGATGTGCAAGAACGACGACGCA 681  
Db 460 GTGCTCCAGTCGGCCCTCGAGAAAGCGAGTCACCCCATGTGCAAGGACGACGAGATGA 519  
QY 682 GAAGATCAACATCTACTGTCTCACGTGTGAGGTGCCTACTTGTCTCTTGTGCAAGGTGTT 741  
Db 520 GAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACTGCTCATGTGCNAGGTGTT 579  
QY 742 TGGGGCTCACAGGCTGTGAGGTTGCCCTTTGCAAGCATCTTCCAAGGACAGAAAGAC 801  
Db 580 TGGGATCCACAGGCTGTGAGGTGCCCATTTGCAGAGTGTCTTCCAGGGACAAAAGAC 639  
QY 802 TGAGCTGAGTCACTGATCTCCATGTGTGTGGGGGAAGCAGCCGATGCAGACGATCAT 861  
Db 640 TGAATCGAATACTGTATCTCCATGTGTGTGGGGGAATGACCGGTGTGCAGACCATCAT 699  
QY 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAAATAGCCACAGGTGAAGGAGGA 921  
Db 700 CACTCAGCTGGAGGATTCCTCGAGTGACCAAGGAGAACAGTCCACAGGTAAAGGAAGA 759  
QY 922 GCTGAGTCAAGAGTTTGCACCCCTCTACGCCATCTCTGAGTGAAGAAAGAGCGAGCTGCT 981  
Db 760 GCTGAGCCAGAAGTTTGCACAGCTTGTATGCCATCTCTGGATGAGAAAGAGTGAAGTGTCT 819  
QY 982 GCAGCGGATCACGACGAGCAGGAGGAGAGCTGGGCTTCATCGAGGCTCTGATCCTCCA 1041  
Db 820 GCAGCGGATCACGACGAGCAGGAGGAGAAAGCTTATGCTTCATCGAGGCGCTCATCCAGCA 879  
QY 1042 GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA 1101  
Db 880 GTACAGGAGCAGCTGGACAGTCCACCAAGCTGTTGGAACTGCCATCCAGTCCCTGGA 939  
QY 1102 TGAGCCCGAGGGGCTACCTCTCTCAAGTGCACAGAGCTCATCAAGAGCATTTGAGA 1161  
Db 940 CGAGCCTGGGGAGCCACCTTCTCTTGACTGCAAGCAACTCATCAAAAGCATTTGTGA 999  
QY 1162 AGCTCCAAAGGCTGCAGCTGGGGAAGACAGAGAGCTTTGAGAAATGAGCTACTT 1221  
Db 1000 AGCTTCAAGGGCTGCAGCTGGGGAAGACAGAGAGGCTTTGAGAAATGAGCTACTT 1059  
QY 1222 TACTTGGACTTAGAACACATAGCAGAGCGCTTTGAGGGCCATTGACTTTGGGACAGGTA 1281  
Db 1060 TACTTTGGATTAGACACATAGCAGACGCCCTGAGAGCCATTGACTTTGGGACAGATGA 1119  
QY 1282 AGGATGTGATG 1292  
Db 1120 GGAAGAGGAAG 1130

RESULT 8

AAS25842  
ID AAS25842 standard; cDNA; 1781 BP.  
XX  
AC AAS25842;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human cDNA encoding a novel secreted protein, Seq ID 21.  
XX  
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;  
KW cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective;  
KW antibacterial; virocid; fungicide; ophthalmological; vulnerary;  
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;  
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
KW cerebral ischaemia; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; epithelial cell proliferation; skin ageing; food additive;  
XX preservative; antiproliferative.  
OS Homo sapiens.  
XX

PN WO200155322-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001341.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.



Db	562	TGGGATCCACAAGGCTGCGAGGTGGCCCCCATTTGCAGAGTGTCTTCCAGGGACAAAAGAC	621	PR	26-JUL-2000; 2000US-0220963P.
Qy	802	TGAGCTGAGTAATGCTCATCTCCATCTGCTGGTGGCGGGGAAACGACCGAGTGCAGACGATCAT	861	PR	26-JUL-2000; 2000US-0220964P.
Db	622	TGAACTGTAATAATGTATCTCCATCTGCTGGTGGCGGGGAATGACCGTGTGCAGACCATCAT	681	PR	14-AUG-2000; 2000US-0224518P.
Qy	862	CTTCTAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAAATAGCCACAGGTGAAGGAGGA	921	PR	14-AUG-2000; 2000US-0224519P.
Db	682	CACCTAGCTGGAGGATTCCTCGTGCAGTGACCAAGGAGAAACAGTCCACCGTAAAGGAAGA	741	PR	14-AUG-2000; 2000US-0225267P.
Qy	922	GCTGAGTCCAGAGTTTGACACCCCTCTACGCCATCTCGCATGAGAAAGAGCGAGCTGCT	981	PR	14-AUG-2000; 2000US-0225268P.
Db	742	GCTGAGCCAGAAGTTTGACACGTTGTATGCCATCTCGATGAGAAAGAGTGAAGTTGCT	801	PR	14-AUG-2000; 2000US-0225270P.
Qy	982	GCAGCGGATCACGACGAGCAGGAGGAGAAAGCTTGGGCTTCATCGAGGCTCTGATCCTCCA	1041	PR	14-AUG-2000; 2000US-0225757P.
Db	802	GCAGCGGATCACGACGAGCAGGAGGAGAAAGCTTAGCTTCATCGAGGCCCTCATCCAGCA	861	PR	14-AUG-2000; 2000US-0225758P.
Qy	1042	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTTGTGGAGACCGCCATCCAGTCCCTGGA	1101	PR	22-AUG-2000; 2000US-0226868P.
Db	862	GTACCAGGAGCAGCTGGACAAGTCCACAAGCTGGTGGAAACTGCCATCCAGTCCCTGGA	921	PR	30-AUG-2000; 2000US-0228924P.
Qy	1102	TGAGCCCGAGGGCTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTGAGA	1161	PR	01-SEP-2000; 2000US-0229287P.
Db	922	CGAGCCTGGGGAGGCACCTTCTCTTGACTGCCAAGCAACTCATCAAAAGCATTTGGA	981	PR	01-SEP-2000; 2000US-0229343P.
Qy	1162	AGCTCCAAAGGGCTGCAGCTGGGGAAGACAGACAGCAAGGCTTTGAGAAATATGGACTACTT	1221	PR	01-SEP-2000; 2000US-0229345P.
Db	982	AGTTCCAAAGGGCTGCAGCTGGGGAAGACAGACAGCAAGGCTTTGAGAAATATGGACTACTT	1041	PR	05-SEP-2000; 2000US-0229509P.
Qy	1222	TACTCTGGACTTAGAACACATAGCAGAGCGCCTTTGAGGGCCATTGACTTTGGGACAGGTAA	1281	PR	05-SEP-2000; 2000US-0229513P.
Db	1042	TACTTTGGATTTAGAGCACATAGCAGACGCGCTTGAGAGCCATTGACTTTGGGACAGATGA	1101	PR	08-SEP-2000; 2000US-0231413P.
Qy	1282	AGGATGTGATG 1292		PR	21-SEP-2000; 2000US-0234223P.
Db	1102	GGAAGAGGAAG 1112		PR	21-SEP-2000; 2000US-0234274P.
RESULT 9				PR	25-SEP-2000; 2000US-0234997P.
ABX73183				PR	27-SEP-2000; 2000US-0235834P.
ID ABX73183 standard; DNA; 1781 BP.				PR	29-SEP-2000; 2000US-0236327P.
XX AC ABX73183;				PR	29-SEP-2000; 2000US-0236367P.
XX DT 18-MAR-2003 (first entry)				PR	29-SEP-2000; 2000US-0236368P.
XX DE Human novel polynucleotide #11.				PR	29-SEP-2000; 2000US-0236370P.
KW Human; gene; db; neural disorder; immune system disorder; renal disorder;				PR	02-OCT-2000; 2000US-0237037P.
KW muscular disorder; respiratory disease; reproductive disorder;				PR	02-OCT-2000; 2000US-0237038P.
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;				PR	02-OCT-2000; 2000US-0237039P.
KW hyperproliferative disorder; inflammatory disease; allergic reaction;				PR	02-OCT-2000; 2000US-0237040P.
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;				PR	13-OCT-2000; 2000US-0239935P.
KW cardiovascular; nephrotropic; cytostatic; antiarteriosclerotic;				PR	20-OCT-2000; 2000US-0240960P.
XX haemostatic; antiarteriosclerotic.				PR	20-OCT-2000; 2000US-0241785P.
XX OS Homo sapiens.				PR	20-OCT-2000; 2000US-0241809P.
XX PN US2002132753-A1.				PR	01-NOV-2000; 2000US-0244617P.
XX PD 19-SEP-2002.				PR	17-NOV-2000; 2000US-0249299P.
XX PF 17-JAN-2001; 2001US-00764864.				PR	08-DEC-2000; 2000US-0251856P.
XX PR 31-JAN-2000; 2000US-0179065P.				PR	08-DEC-2000; 2000US-0251868P.
PR 04-FEB-2000; 2000US-0180628P.				XX	
PR 28-JUN-2000; 2000US-0214886P.				PA	(ROSE/) ROSEN C A.
PR 07-JUL-2000; 2000US-0216647P.				PA	(RUBE/) RUBEN S M.
PR 07-JUL-2000; 2000US-0216880P.				XX	(BARA/) BARASH S C.
PR 11-JUL-2000; 2000US-0217487P.				PI	Rosen CA, Ruben SM, Barash SC;
PR 11-JUL-2000; 2000US-0217496P.				XX	WPI; 2003-147444/14.
PR 14-JUL-2000; 2000US-0218290P.				DR	P-PSDB; ABU54923.
				DR	
				XX	
				CC	The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent

(ROSE/) ROSEN C A.  
(RUBE/) RUBEN S M.  
(BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-147444/14.  
P-PSDB; ABU54923.

New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.

Claim 1; SEQ ID NO 21; 402pp; English.

The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, congenital heart defects, Ebsstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent

CC	human novel polynucleotides of the invention	
XX		
SQ	Sequence 1781 BP; 494 A; 399 C; 511 G; 377 T; 0 U; 0 Other;	
	Query Match 49.9%; Score 797.4; DB 8; Length 1781;	
	Best Local Similarity 85.8%; Pred. No. 5.1e-202;	
	Matches 885; Conservative 0; Mismatches 146; Indels 0; Gaps 0;	
QY	262 GACGAGCTGGGCAAGACAGATCGCATTTTCAAGCAATATGGATTATAAATCTAGCCTGAT 321	Db 1042 TACTTTGGATTAGAGCACATAGCAGACGCCCTTGAGCCATTGACTTTGGACAGATGA 1101
Db	82 GAGGAGCTAGCGTGGCTCTATTCTTCCACAGAAATGGATTATAAGTCGAGCCTGAT 141	QY 1282 AGGATGTGATG 1292
QY	322 TCCTGATGAAGACGCTATGAGAACTGGAGAGCAGCTGATCTGCCCATCTGCTGGA 381	Db 1102 GGAAGAGGAG 1112
Db	142 CCAGGATGGGAATCCCATGGAGAACTTGAGAGCAGCTGATCTGCCCTATCTGCTGGA 201	
QY	382 GATGTTTACCAAGCTGTGGTCACTCTGCCCTGCCAACAACACCTCTGCCGGAAGTGTGC 441	RESULT 10
Db	202 GATGTTTACCAAGCAGTGTGTCATCTGCGCTGCCAGCAACCTCTGCGGGAAGTGTGC 261	ABS70380
QY	442 CAACGACATCTTCCAGGCTCGGAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 501	ID ABS70380 standard; cDNA; 1757 BP.
Db	262 CAATGACATCTTCCAGGCTGCAATCCCTACTTGGACCAACCGCGGCGAGCTCAGTGTCCAT 321	XX ABS70380;
QY	502 GTCTGAGGTGCTTCCGTTGCCCTCTGTCGCCCATGAAAGTATCATGGACCGGACGCG 561	AC ABS70380;
Db	322 GTCTGAGGCGCTTTCGCTGCCCACTCTGCCCAACGAGGTGATCATGGATCGTCAAGG 381	DT 27-NOV-2002 (first entry)
QY	562 GGTGTACGCGCTGCAGAGAACTCTGCTGTGAAACATCATTTGACATCTACAAGCAGA 621	DE Human bone remodelling gene #37.
Db	382 AGTTTACGCGCTGCAGAGAACTCTGCTGTGAAACATCATTCGACATCTACAAGCAGA 441	XX Bone remodelling; osteoporosis; human; gene; ss.
QY	622 GTGCTCCAGTCCGCGCTTCAGAAAGGACGACCCCGATGTGCAAGGAACACGAAGACGA 681	OS Homo sapiens.
Db	442 GTGCTCCAGTCCGCGCTTCAGAGGACGACCCCGATGTGCAAGGAACACGAAGATGA 501	XX US6426186-B1.
QY	682 GAAGATCAACATCTACTGTCTCAGTGTGAGTGTCTACTTGTCTTGTGCAAGGTGT 741	PD 30-JUL-2002.
Db	502 GAAAAATAACATCTACTGTCTCAGTGTGAGTGTCTACTTGTCTTGTGCAAGGTGT 561	PF 18-JAN-2000; 2000US-00484970.
QY	742 TGGGGCTACCAAGGCTGTGAGGTGCGCTTTCGAAGCATCTTCCAGGACACGAGAC 801	PR 18-JAN-2000; 2000US-00484970.
Db	562 TGGGATCCAAAGGCTGTGAGGTGCGCTTTCGAAGCATCTTCCAGGACACGAGAC 621	XX (INCY-) INCYTE GENOMICS INC.
QY	802 TGAGCTGAGTAACTGTCATCTCCATGTGTTGGGGGGAACGACCGAGTGCAGACCATCAT 861	XX Jones KA, Volkmut W, Walker MG;
Db	622 TGAATCTGATATCTGATCTCTATCTGTTGGGGGGAATGACCGTGTGCAGACCATCAT 681	XX WPI: 2002-673014/72.
QY	862 CTCTCAGCTGGAGGACTCTGTGAGAGTGACCAAGAGAAATAGCCACGAGTGAAGAGA 921	DR P-PSDB; ABG93804.
Db	682 CACTCAGCTGGAGGATTCCTCGAGTGACCAAGAGAAACAGTCAACAGGTAAAGGAAGA 741	XX A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful in an array for the diagnosis of bone remodeling and osteoporosis associated disorders.
QY	922 GCTGATCAGAGTTGTGACACCTCTACCCATCTGGATGAGAGAGAGCGAGCTGCT 981	XX Claim 1; Col 135-138; 206pp; English.
Db	742 GCTGAGCCAGAGTTGTGACACCTGTGATGCCATCTGGATGAGAGAAAGTGTGCT 801	XX The invention relates to a combination comprising a number of CC substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodeling and CC osteoporosis. The invention is used to diagnose disorders associated with CC bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone remodelling genes of the invention
QY	982 GCAGCGGATCAGCAGGAGCAGAGAGAGTGGGCTTTCATCGAGGCTCTCATCTCTCA 1041	XX Query Match 46.8%; Score 747.8; DB 6; Length 1757;
Db	802 GCAGCGGATCAGCAGGAGCAGAGAGAAAGTGTGATCTTCCAGGCGCTCATCCAGCA 861	Best Local Similarity 82.8%; Pred. No. 8.8e-189;
QY	1042 GTACAGGAGAGCTGGAAGATCCAAAGCTTGTGGAGACCGGCATCCAGTCCCTGGA 1101	Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
Db	862 GTACAGGAGAGCTGGAAGATCCAAAGCTTGTGGAGAACTGCGCATCCAGTCCCTGGA 921	QY 262 GACGAGCTGGGCAAGACAGATCGCATTTTCAAGCAATATGGATTATAAATCTAGCCTGAT 321
QY	1102 TGAGCCGAGGAGGCTTACCTCTCTCAGTCCAGCAGCTCATCAAGAGCATTTGTAGA 1161	Db 88 GAGGAGCTAGCGTGGCTCTCTTCTTCCACAGAAATGGATTATAAGTCGAGCCTGAT 147
Db	922 CGAGCCTCGGGGAGGCCCTTCTCTTGTACTGCAAGCAACTCATCAAAAGCATTTGTGA 981	QY 322 TCCTGATGGAACGCTATGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTGCTGGA 381
QY	1162 AGCCTTCAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTTTGAAACATGGAATCTT 1221	Db 148 CCAGGATGGGAATCCCATGGAGAACTTGGAGAGCAGCTGATCTGCCCTATCTGCTGGA 207
Db	982 AGCTTCAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTTTGAAACATGGAATCTT 1041	QY 382 GATGTTTACCAAGCTGTGGTCACTCTGCCCTGCCAACAACACCTCTGCCGGAAGTGTGC 441
QY	1222 TACTCTGGAATTAGAACACATAGCAGAGGCGCTTGGAGGCCATTTGACTTTGGGACAGGTAA 1281	Db 208 GATGTTTACCAAGCAGTGGTCACTTTCGCTGCCAGCACAACCTGTGCCGGAAGTGTGC 267
		QY 442 CAACGACATCTTCCAGGCTGGGAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 501
		Db 268 CAATGATATTTTCCAGGCTCTTAACCCGTATTTTGGCCCAAGAGGAGGTACCAACCATGGC 327



Db 328 ATCAGGGGCGCAATTCGCTGCCATCCTGTAGACATGAAGTGGTTTGGATAGACATGG 387  
Qy 562 GGTGTACCGCTGACAGAGGAACCTCTGCTGGTGAAGAACATCATTTGACATCTACAAGCAGGA 621  
Db 388 GGTATATGACTTCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAACAGGA 447  
Qy 622 GTGCTCCAGTGGCCCTGACAGAAAGGAGCCACCGGATGTGCAAGAACACAGAGAGGA 681  
Db 448 GTGCTCCAGTGGCCCTGACAGAAAGGAGCTCACCCCATGTGCAAGGAGCAGCAAGATGA 507  
Qy 682 GAAAGATCAACATCTACTGTCTCACGTGTGAGGTGCTACTTCTCTGTGCAAGGTGTT 741  
Db 508 GAAATCAACATCTACTGTCTCACGTGTGAGGTGCCACCTGCTCATGTGCAAGGTGTT 567  
Qy 742 TGGGGCTCACAGGCGCTGTAGGTGGCCCTTTGCAAAAGCATCTTCCAAGGACAGAAAGC 801  
Db 568 TGGGATCCACAAGGCTGCGAGGTGGCCCATTTGCAGAGTGTCTCCAGGGACAAAAGC 627  
Qy 802 TGAGCTGAGTAACTGATCTCCATGCTGTGGTGGGGAGACGACCGAGTGCAGACATCAT 861  
Db 628 TGAATCTGAATACTGTATCTCCATGCTGGTGGGGGAATGACCGGTGTGCAGACCATCAT 687  
Qy 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAAATAGCCACAGGTGAAGGAGGA 921  
Db 688 CACTCAGCTGGAGGATTCCTGCTGAGTGACCAAGGAGAACTCACCAGGTAAAGGA 747  
Qy 922 GCTGAGTCAGAAAGTTTGACACCTCTTACGCCATCTCTGGATGAGAAAGAGCGAGCTGT 981  
Db 748 GCTGAGCCAGAAAGTTTGACACCTTGTATGCCATCTCTGGATGAGAAAGAGTGTGTCT 807  
Qy 982 GCAGGGATCAGCAGGAGCAGAGGAGAGAGCTGGCTTCATCGAGGCTCTGATCTCTCA 1041  
Db 808 GCAGGGATCAGCAGGAGCAGAGGAGAAAGCTTAGCTTTCATCGAGGCTCTCATCCAGCA 867  
Qy 1042 GTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCATCCAGTCCCTGGA 1101  
Db 868 GTACAGGAGCAGCTGGAGAGTCCAAAGCTGTGGAACTGCATCCAGTCCCTGGA 927  
Qy 1102 TGAGCCGAGGGGCTTACCTCTCTCAAGTCCCAAGCAGCTCATCAAGAGCATTTGTAGA 1161  
Db 928 CGAGGCTGGGGAGCCACCTCTCTTGTACTGCCAAGCAACTCATCAAAAGCATTTGTGA 987  
Qy 1162 AGCTTCCAAAGGCTGCGAGCTGGGAGACAGACAGCAAGGCTTTGAGAACATGGACTACTT 1221  
Db 988 AGCTTCCAAAGGCTGCGAGCTGGGAGACAGACAGCAGGCGCTTTGAGAACATGGACTTCT 1047  
Qy 1222 TACTCTGGACTTAGAACACATAGCAGAGGCTTTGAGGGCATTTGAGGACAGGTAA 1281  
Db 1048 TACTTTGGATTAGACACATAGCAGAGCGCTTGAGAGCCATTTGAGGACAGATGA 1107  
Qy 1282 AGGATGTGATG 1292  
Db 1108 GGAAGGGAAG 1118  
RESULT 12  
ID AAH89924  
XX AAH89924 standard; cDNA; 1796 BP.  
AC AAH89924;  
XX  
XX 01-OCT-2001 (first entry)  
DT Human bone marrow cDNA, SEQ ID NO: 55.  
DE  
DE Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;  
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;  
KW immunosuppressive; gene therapy; cytokine cell proliferation;  
KW cell differentiation modulator; immune disorder; infection; cancer;  
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.  
OS Homo sapiens.  
XX

PN WO200153453-A2.  
XX  
PD 26-JUL-2001.  
XX  
PF 23-DEC-2000; 2000WO-US034960.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-0052317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 30-NOV-2000; 2000US-0250583P.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;  
PI Ren F, Wang J, Wethman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Drmanac RT;  
XX  
DR WPI: 2001-488707/53.  
DR P-PSDB; AAM00805.  
XX  
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful for  
PT treating e.g. cancer and immune deficiency disorders.  
XX  
PS Claim 1; Page 243-244; 648pp; English.  
XX  
CC The present sequence is one of 251 novel human polynucleotides expressed  
CC in the bone marrow. The polynucleotide and the polypeptide encoded by it  
CC are useful in the treatment of various immune deficiencies and disorders.  
CC The deficiencies and disorders may be genetic, may be caused by a viral  
CC (e.g. HIV), bacterial or fungal infection, or may result from an  
CC autoimmune disorder, a coagulation disorder (e.g. haemophilia)  
CC inhibition of tumour cell proliferation, suppression of an inflammatory  
CC response or treatment of a nervous system disorder such as Alzheimer's  
CC disease. Detection of the presence or increased expression of the  
CC polynucleotide or the protein it encodes is useful for the diagnosis  
CC and/or prognosis of one or more types of cancer. The polynucleotide and  
CC polypeptide can be used as nutritional sources or supplements and in the  
CC screening of chemical compounds as potential drugs  
XX  
SQ Sequence 1796 BP; 449 A; 420 C; 490 G; 390 T; 0 U; 47 Other;  
Query Match 42.6%; Score 679.8; DB 5; Length 1796;  
Best Local Similarity 81.6%; Pred. No. 1.2e-170;  
Matches 850; Conservative 0; Mismatches 184; Indels 8; Gaps 8;  
Qy 295 CAATATGGATTATAAATCTAGCCTGATTCC-TGATGGAAACGCTATGGAGAACCTGGAGA 353  
Db 146 CAGAACGGACTATAAGTCGAGCCTGACTCCAGGATGGGAATCCCATGGAGAACTTGGAGA 205  
Qy 354 AGCAGCTGATTCGCCCATCTGCTGGAGAGA-TGTTTACCAAGCCTGTGGTCACTCTGCC 412  
Db 206 TGCAGCTGATTCGGCTTATCTGCCCGAGATTGTGTACCAAGCCGCTGTGTCTCTGCCG 265  
Qy 413 TGCACACACACCTCTGCGGGAAGTGC-CAACACACATCTTCCAGGCTGCCAATCCCTTA 471  
Db 266 TGCCAGCACAACCTGTGCGGGAAGTGTCTCAATGACATCTTCCAGGCTGCAATATCCCTA 325  
Qy 472 CTGGACCAACCGCGGTGGCTCAGTGTCCATGTCTGGAGGTGCTTTCCGTTGCCCTCTG 531  
Db 326 CTGGACCAACCGCGGCGAGCTCAGTGTCCATGTCTCGAGGTGCTTTCCGCTGCCACCTG 385  
Qy 532 CGCCCATGAGTGTATGTGACCGGACGCGGAGTGA-CGGCTCGAGAGGAACCT-TGCTG 589  
Db 386 CGCCACGAGGTGTATGTGATCGTACGCGAGTGTACCGTGTGTGACAGGAACCTTTGTTG 445  
Qy 590 GTGGAAACATCATTTGACATCTTACAAGCAGGAGTGC-TCCAGTCCGCGCCCTCAGAAAGG 648  
Db 446 GTGGAAACATCATCGACATCTTACAAGCAGGAGTGTCTTCCAGTCCGCGCCCTCAGAAAGC 505





QY 682 GAAGATCAACTACTTCTCAGCTGAGAGTGGCTACTTCTCTTGTGCAAGGTGT 741  
 DB 540 GAAATCAACTACTTCTCAGCTGAGAGTGGCTACTTCTCTTGTGCAAGGTGT 599  
 QY 742 TGGGGCTCACCAGGCTGTGAGTTGGCCCTTTGCAAGCATCTTCCAGGACAGAC 801  
 DB 600 TGGGATCCACAAGGCTGCGAGTGGCCCATTTGCAGAGTGTCTTCCAGGGACAAAAGAC 659  
 QY 802 TGAGCTGAGTAAGTCTCAGTCTGCTGCTGGCGGGAACGACGAGTGCAGCATCAT 861  
 DB 660 TGAATGATTAAGTCTCAGTCTGCTGCTGGCGGGAATGACCTGTGCGACCATCAT 719  
 QY 862 TCTCAGCTGAGGAGTCTGCTGAGAGTACCAAGAGAGTACCCACGAGTGAAGAGGA 921  
 DB 720 CACTCAGCTGAGGAGTCTGCTGAGTACCAAGAGAGTACCCACGAGTGAAGAGGA 779  
 QY 922 GCTGAGTCAAGTCTGAGCCTCTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 981  
 DB 780 GCTGAGCCAGAAAGTTTGACACCTTGTATGCCATCTGCTGCTGCTGCTGCTGCTGCT 839  
 QY 982 GCAGCGGATCAGCAGGAGCAGGAGAGAGTGGGCTTCTGAGGCTCTGATCTCCA 1041  
 DB 840 GCAGCGGATCAGCAGGAGCAGGAGAGAGTGGGCTTCTGAGGCTCTGATCTCCA 899  
 QY 1042 GTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTGAGACCGCATCCAGTCCCTCGA 1101  
 DB 900 GTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTGAGACCGCATCCAGTCCCTCGA 959  
 QY 1102 TGAGCCCGAGGGGCTACCTTCTCT 1127  
 DB 960 CGAGCTGGGGAGCCACCTTCTCT 985

RESULT 14  
 ABQ79510  
 ID ABQ79510 standard; DNA; 630 BP.  
 XX  
 AC ABQ79510;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Rat MURF1 VRV splice form encoding DNA.  
 XX  
 KW Muscle atrophy protein; MURF1; MURF3; MAFBX; atrophy; neuroprotective;  
 KW gene therapy; transgenic; gene; rat; ds.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..630  
 FT /\*tag= a  
 FT /product= "MURF1 VRV splice form"  
 FT /partial  
 FT /note= "the start and stop codons are not indicated"  
 XX  
 PN WO200261046-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 30-JAN-2002; 2002WO-US002811.  
 XX  
 PR 30-JAN-2001; 2001US-0264926P.  
 PR 10-AUG-2001; 2001US-0311697P.  
 PR 22-OCT-2001; 2001US-0338742P.  
 XX  
 XX (REG-) REGENERON PHARM INC.  
 PA Glass DJ, Bodine SC;  
 XX  
 PI WPI: 2002-608513/65.  
 DR P-PSDB; ABB81142.  
 DR  
 XX Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g.

PT MURF1, MURF3 or MAFBX, useful for treating muscle atrophy and other  
 PT related disorders, e.g. Guillain-Barre syndrome, peripheral neuropathy,  
 PT and nerve damage.  
 XX  
 PS Claim 3; Fig 16; 104pp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules encoding muscle  
 CC atrophy proteins MURF1, MURF3, or MAFBX. The proteins can be expressed by  
 CC standard recombinant methodology. The nucleic acid molecules and  
 CC polypeptides are useful for treating muscle atrophy or detecting atrophy,  
 CC and for treating related diseases/disorders, e.g. Guillain-Barre  
 CC syndrome, peripheral neuropathy, or nerve damage caused by environmental  
 CC toxins or drugs. The MURF1, MURF3 and MAFBX antagonists, and the  
 CC antagonists of their pathways are useful for inhibiting atrophy, inducing  
 CC hypertrophy, decreasing ubiquitination, interfering with the ubiquitin  
 CC pathway, or modulating MURF1, MURF3 or MAFBX expression or activity. The  
 CC nucleotide sequences are useful for diagnostic and genetic testing. The  
 CC present sequence represents a rat MURF1 VRV splice form encoding DNA  
 XX  
 SQ Sequence 630 BP; 153 A; 175 C; 173 G; 129 T; 0 U; 0 Other;  
 Query Match 34.3%; Score 547.4; DB 6; Length 630;  
 Best Local Similarity 94.0%; Pred. No. 1.7e-135;  
 Matches 569; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
 QY 295 CAATATGATTAATAATCTAGCTGATTCCTGATGGAACGCTATGGAGAACCTGGAGAA 354  
 DB 21 CGACAAGATTATAATCTGCTTGGATTCGAGCGAAGATGCTATGGAGAACCTGGAGAA 80  
 QY 355 GCAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCTGTGGTATCTCTGCCCTG 414  
 DB 81 GCAGCTCATCTGCCCATCTGCTTGGATGTTTACCAAGCTGTGGTATCTCTGCCCTG 140  
 QY 415 CCAACACACCTCTGCGGGAAGTGTCCAAAGCATCTTCCAGGCTGCGAATCCCTACTG 474  
 DB 141 CCAGCAACACCTCTGCGGGAAGTGTCCAAAGCATCTTCCAGGCTGCGAATCCCTACTG 200  
 QY 475 GACCAACCGCGGTGGCTCAGTGTCCATGTCTGGAGTGGTTCCTGTCGCCCTCGTCCG 534  
 DB 201 GACCAACCGCGGTGGCTCAGTGTCCATGTCTGGAGTGGTTCCTGTCGCCCTCGTCCG 260  
 QY 535 CCATGAAGTATGATGAGACCGGCGACGGGTGTACGGCTGCGAGAGAACCTCTGGTGA 594  
 DB 261 CCATGAAGTATGATGAGACCGGCGATGGGTGTACGGTCTGCGAGAGAACCTCTGGTGA 320  
 QY 595 AAACATCATTCGACATCTACAAGCAGAGTGTCTCCAGTCCGCCCTGCGAAGAGGAGCCA 654  
 DB 321 GAACATCATTCGACATCTACAAGCAGAGTGTCTCCAGTCCGCCCTGCGAAGAGGAGCCA 380  
 QY 655 CCCGATGTGCAAGGAACACGAGAGCAGAGATCAACATCTACTGTCTCACGTGTGAGGT 714  
 DB 381 CCCGATGTGCAAGGAACACGAGAGCAGAGATCAACATCTACTGTCTCACGTGTGAGGT 440  
 QY 715 GCCTACTTGTCTCTTGTGCAAGGTGTGGGTGTCCAGGCTGCGAGGCTGTGAGGTGGCCCTTT 774  
 DB 441 GCCTACTTGTCTCTTGTGCAAGGTGTGGGTGTCCAGGCTGCGAGGCTGTGAGGTGGCCCTTT 500  
 QY 775 GCAAGAGCATCTTCCAAAGGACAGAGACTGAGTGTAGTAATCTCATCTCTCATCTGTGTGC 834  
 DB 501 ACAAAGCATCTTCCAAAGGACAGAGACTGAGTGTAGTAATCTCATCTCTCATCTGTGTGC 560  
 QY 835 GGGGAACGACCGAGTGTGAGAGCATCATCTCTCAGCTGGAGGACTGTGTCAGAGTACCAA 894  
 DB 561 AGGGAACGACCGAGTGTGAGAGCATCATCTCTCAGCTGGAGGACTGTGTCAGAGTACCAA 620  
 QY 895 GGAGA 899  
 DB 621 GGTGA 625  
 RESULT 15  
 ABA99061  
 ID ABA99061 standard; DNA; 1431 BP.



XX Homo sapiens.  
OS WO2003029271-A2.  
PN 10-APR-2003.  
XX 24-SEP-2002; 2002WO-US030474.  
XX 24-SEP-2001; 2001US-0324631P.  
XX (HYSE-) HYSEQ INC.  
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;  
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Wang G;  
PI Haley-Vicente D, Drmanac RT;  
XX WPI; 2003-371981/35.  
DR P-PSDB; ADC31154.  
XX New polynucleotide and polypeptide useful for diagnosing, preventing or  
PT treating conditions such as neurodegenerative diseases, anemias, platelet  
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
PT cancer.  
XX Claim 1; SEQ ID NO 265; 1185pp; English.  
XX The invention relates to 971 novel human cDNA sequences (ADC29919-  
CC ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The  
CC invention also relates to nucleic acid sequences over 99% identical with  
CC the novel human cDNAs. The invention additionally encompasses expression  
CC vectors and host cells comprising a nucleic acid of the invention; the  
CC recombinant production of a polypeptide of the invention; an antibody  
CC against a polypeptide of the invention; a method of detecting  
CC polynucleotides or polypeptides of the invention; and methods of  
CC identifying a compound which binds to a polypeptide of the invention. The  
CC invention further discloses methods of preventing, treating or  
CC ameliorating a medical condition; kits comprising polynucleotide probes  
CC and/or monoclonal antibodies for carrying out the methods of the  
CC invention; methods for the identification of compounds that modulate the  
CC expression or activity of the polynucleotide and/or polypeptide; and 767  
CC contig sequences corresponding to the cDNA sequences of the invention  
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628  
CC -ADC33394). The nucleic acids and polypeptides of the invention are  
CC useful in diagnostics, drug screening, forensics, gene mapping, in the  
CC identification of mutations responsible for genetic disorders or other  
CC traits, for assessing biodiversity, and in producing many other types of  
CC data and products dependent on DNA and amino acid sequences. They are  
CC also used for treating diseases such as Parkinson's disease, Alzheimer's  
CC disease and other neurodegenerative diseases, anaemia, platelet  
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
CC cancer. The nucleic acids may also be used as hybridisation probes or  
CC primers, and in the recombinant production of a protein. The polypeptides  
CC are also useful in generating antibodies, as molecular weight markers,  
CC and as food supplements. The present sequence represents a specifically  
CC claimed human cDNA sequence of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1405 BP; 353 A; 360 C; 462 G; 230 T; 0 U; 0 Other;  
Query Match 30.2%; Score 481.8; DB 10; Length 1405;  
Best Local Similarity 69.4%; Pred. No. 7.7e-118;  
Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;  
QY 317 CTGATTCTCGATGGAAACCGCTATGGAGAACCTGGAGAACGACTGATCTGCCCATCTGCG 376  
DB |||||  
DB 313 CTGCTAGGGGATGCACACAGCATGGACACCTGGAGAACGACTCATCTGCCCATCTGCG 372  
QY 377 CTGGAGATGTTTACCAAGCTGTGTCATCTCCCTGCGCAACACACACTCTGCGCGAAG 436  
DB |||||  
DB 373 CTGGAGATGTTTCTCCAAACCAAGTGTGATCTCTGCGCCCTGCGCAACACCAACCTGTGCGCGCAA 432

QY 437 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTCGAACCAACCGGGTGGCTCAGTG 496  
DB |||||  
DB 433 TGTGCCAACGACGCTTCTCCAGGCTGCGAATCCCTATATGGCAGTCCCGGGCTCCACCACT 492  
QY 497 TCCATGCTCGAGGTCGTTTCGGTTGCCCTCGTGCAGCCCATGAAGTATCATGAGCCGG 556  
DB |||||  
DB 493 GTGTCTTCAGGAGCCGTTTCCGCTGCCCATCGTGCAGGCGATGAGGTTGTCTCGACACA 552  
QY 557 CACGGGTGTACCGGCTGCAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTACAAAG 616  
DB |||||  
DB 553 CACGGTGTCTACGGCTGCAGGAAACCTGCTAGTGGAGAACATTTATCGACATTTACAAAG 612  
QY 617 CAGGAGTCTCCAG---TCGGCCCTGCAGAAAGCAGCCACCCGATGTGCAAGAAACAC 673  
DB |||||  
DB 613 CAGGAGTCTATCCAGCCGCTGCACCTCCAAAGGCTGAGCAGCACCTCATGTGCGAGGAGCAT 672  
QY 674 GAAGCAGAAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTTGTCTCTTGGC 733  
DB |||||  
DB 673 GAAGAAGAGAGATCAATATTTACTGCTGAGCTGTGAGGTGCCACCTGTCTCTCTGCG 732  
QY 734 AAGGTGTTTGGGCTCACAGCCCTGTGAGGTGGCCCTTTTGCAAAGCATCTTCAAGAGA 793  
DB |||||  
DB 733 AAGGTCTTGGTGGCCCAAGGACTGTGAGGTGGCCCACTGCCCACCATTTACAAAGC 792  
QY 794 CAGAAGACTGAGCTGAGTAACCTGCATCTCCATGTGTGGCGGGGAAACGACGAGTGCAG 853  
DB |||||  
DB 793 CAGAAGAGTGAAGTCTCAGCGATGGCATCGCATGCTGTGTGGCAGGCAATGACCGCTGCAA 852  
QY 854 AGCATCATCTCTCAGCTGAGGACTCTGTCAGAGTGACCAAGGAGAAATAGCACCAGGTG 913  
DB |||||  
DB 853 GCAGTGAATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACAATAGCCGAGGCG 912  
QY 914 AAGGAGGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCTCTGATGAGAAAGAGC 973  
DB |||||  
DB 913 AAGCAGTTGTTAAACACAGGTTTGAAGCTGTGCGCAGTCTGAGGAGGCGCAAGGT 972  
QY 974 GAGTGTCTGACGCGGATCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033  
DB |||||  
DB 973 GAGTGTCTGACGCGGCTGCGCCGCGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1032  
QY 1034 ATCTCTCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1093  
DB |||||  
DB 1033 ATCCGTGATGAGTGGCGACCACTTGGAGCCCTCTCTAAGCTGGTGGAGTCTGCCATCC 1092  
QY 1094 TCCCTGAGTACGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153  
DB |||||  
DB 1093 TCCATGGAAGAGCCCAATATGGCGCTGTATCTCCAGCAGGCGCAGGAGGAGGAGG 1152  
QY 1154 ATTGTAGAAGCTCTCAAGGGCTGCCAGCTGGGGAGAGCAGAGCAAGGGCTTTTGGAGAAC 1213  
DB |||||  
DB 1153 GTCCGGGCGCATGTCTGAAGGTGGAGCTGGCAGGGCGCGGAGCCAGGCTATGAGAGCAT 1212  
QY 1214 GACTACTTACTCTGGACTTAGAACACATAGCAGAGGCGCTTGGAGGCGCATTTGACTTGG 1273  
DB |||||  
DB 1213 GAGCAATTTACCGTAAAGGTGGAGCAGCGTGGCCGAAATGCTGCGGAGCCATCGACTTCC 1272  
QY 1274 ACAGG 1278  
DB |||||  
DB 1273 CCAGG 1277

## RESULT 17

AAH68563  
ID AAH68563 standard; cDNA; 1913 BP.  
XX  
AC AAH68563;  
XX  
DT 13-SEP-2001 (first entry)  
XX  
DE Human protein HP01115 coding sequence.  
XX  
KW Human; gene therapy; tumour; ss.

XX	OS	Homo sapiens.	Db	690	GAAGAAGAGAGATCAATATTTACTGCTGAGCTGTGAGGTGCCACCTGCTCTCTCTGC	749
XX	PN	WO200142302-A1.	Qy	734	AAGGTGTTTGGGGCTCACCGGCTGTGAGGTGGCCCTTTGCAAGAGCATCTTCCAGGA	793
XX	PD	14-JUN-2001.	Db	750	AAGGTCTTCGGTGCACCAAGGACTGTGAGGTGGCCCACTGCCCCACCATTTACAACAGC	809
XX	PF	06-DEC-2000; 2000WO-JP008631.	Qy	794	CAGAAGACTGAGCTGAGTAATCTCCATGCTGCTGGTGGCGGGAAACGACCGAGTGCAG	853
XX	PR	06-DEC-1999; 99JP-00346863.	Db	810	CAGAGAGTGAAGTCAAGCATGCGATCGGATGCTGTGGCAGGCAATGACCGCTGCAG	869
XX	PR	06-DEC-1999; 99JP-00346864.	Qy	854	ACGATCATCTCTCAGCTGAGGAGTCTGTGAGAGTGAACCAAGAGATATGACCAACAGGTG	913
XX	PR	08-FEB-2000; 2000JP-00031062.	Db	870	GCACTGATCACACAGATGAGGAGGTGTGCCAGACTTATCGAGGACATATAGCCGAGGCAG	929
XX	PR	10-FEB-2000; 2000JP-00034090.	Qy	914	AGGAGGAGCTGAGTCAGAGTTCGACACCTCTACGCCATCTGATCAGAGGAGAGC	973
XX	PR	14-FEB-2000; 2000JP-00034091.	Db	930	AAGCAGTGTGTTAAACCAAGAGGTGTGAGACCTGTGCGCAGTGTGAGGAGGCGCAAGGGT	989
XX	PR	14-FEB-2000; 2000JP-00035829.	Qy	974	GAGCTGCTCAGCGGATCACGAGGAGCAGGAGGAGGAGGAGTGGGCTTCATCGAGGCTCTG	1033
XX	PR	14-MAR-2000; 2000JP-00071161.	Db	990	GAGCTGCTCAGCGGCTGCGCCCGGAGCAAGAGGAGAGTGCAGCGCTCCGCGGCTC	1049
XX	PR	30-MAY-2000; 2000JP-00160851.	Qy	1034	ATCTCCAGTACAGGAGAGCAGCTGGAAGTCCACCAAGCTTGTGAGAGCCGCGCATCCAG	1093
XX	PI	Kato S, Eguchi C, Saeki M;	Db	1050	ATCCGTGAGTATGGGAGCACCCTGGAGGCTCTCTTAAGCTGGTGGAGTCTGCCATCCAG	1109
XX	DR	WPI; 2001-381646/40.	Qy	1094	TCCTGGATGAGCCGCGGAGGAGGCTACCTTCTCTCAAGTCCCAAGCAGCTCATCAAGAGC	1153
XX	DR	P-PSDB; AAG93278.	Db	1110	TCATGGAAGAGCCCAATGCGCTGTATCTCCAGCAGGCCAAGAGCTGATCAATAAG	1169
XX	PT	Human protein originated from tumor cell line, applicable as drug,	Qy	1154	ATTGTAGAGCCTCCCAAGGGCTGCCAGCTGGGGAGACAGAGCAAGGCTTTTGAGAACATG	1213
XX	PT	reagent for studying intracellular protein networks and protein source	Db	1170	GTCGGGGCCATGTCGAAGGTGGAGCTGGCAGGCGCGCGAGCCAGGCTATGAGAGCATG	1229
XX	PT	for drug screening, also encoded cDNA for gene diagnosis and gene	Qy	1214	GACTACTTTACTCTGAGCTTAGAACAATAGAGGAGGCTTGAAGGCCATTTGACTTTGGG	1273
XX	PT	therapy.	Db	1230	GAGCAATTCACCGTAAGGGTGGAGCAGCTGGCGGCAATGCTGCGGAGCCATCGACTTCCAG	1289
XX	PS	Claim 3; Page 236-240; 471pp; Japanese.	Qy	1274	ACAGG 1278	
XX	SS	The present sequence is a human protein coding sequence. The human	Db	1290	CCAGG 1294	
XX	CC	protein, preferably originated from tumour cell line, is applicable as a				
XX	CC	drug, a reagent for studying intracellular protein networks and a protein				
XX	CC	source for screening proteins for binding low molecular weight drugs. The				
XX	CC	human protein coding sequence is useful for gene diagnosis and gene				
XX	CC	therapy, expression vectors and transformant cells for detection of				
XX	CC	ligands and receptors				
XX	Sequence	1913 BP; 446 A; 537 C; 612 G; 318 T; 0 U; 0 Other;				
Query Match 30.2%; Score 481.8; DB 5; Length 1913;						
Best Local Similarity 69.4%; Pred. No. 8.8e-118;						
Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;						
Qy	317	CTGATTCCTGATGGAAACGCTATGGAAGACCTGGAGAGCAGCTGATCTGCCCTCATCTGC	376			
Db	330	CTGCTAGGGGATGACACAGCATGGACAACCTGGAGAGCAGCTCATCTGCCCTCATCTGC	389			
Qy	377	CTGGAGATGTTTACCAAGCTGTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	436			
Db	390	CTGGAGATGTTTCTCAAAACAGTGGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	449			
Qy	437	TGTGCAACGACATCTTCCAGGCTGGGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG	496			
Db	450	TGTGCAACGACATCTTCCAGGCTGGGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG	509			
Qy	497	TCCATGCTGAGAGTGTGTTCCGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	556			
Db	510	GTGCTTTCAGGAGCGCGTTTCCGCTGCCATCGTGCAGGATGAGGTTTGTCTGGACAGA	569			
Qy	557	CACGGGCTGTACGGCTGACAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	616			
Db	570	CACGGTGTCTACGGCTGACAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	629			
Qy	617	CAGGAGTGTCTCCAG---TGGCGGCTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	673			
Db	630	CAGGAGTGTCTCCAGGCGCTGCACTCCAGGCTGACAGCAGCAGCAGCAGCAGCAGCAGC	689			
Qy	674	GAGAGCAGAGATCAACATCTACTGCTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG	733			

RESULT 18	
AAH78026	
ID	AAH78026 standard; cDNA; 1990 BP.
XX	
AC	AAH78026;
XX	
DT	26-NOV-2001 (first entry)
XX	
DE	Nucleotide sequence of human cardiomyopathy associated protein (CAP).
XX	
KW	Human; cardiomyopathy associated protein; CAP; myocardial biopsy;
KW	left ventricle assist device; LVAD; cardiomyopathy;
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
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CDS	/*tag= a
FT	/product= "cardiomyopathy associated protein (CAP)"
XX	
PN	WO200162767-A1.
XX	
PD	30-AUG-2001.
XX	
PF	26-FEB-2001; 2001WO-US005888.
XX	
PR	24-FEB-2000; 2000US-0184825P.
XX	
PA	(GENE-) GENE LOGIC INC.

XX	Bednarik D, Greene J, White M;	910	AAGCAGTTGTTAAACACGAGGTTTGGAGGCTGTGCGCAGTGTGAGAGCGCAAGGGT	969
PI	WPI; 2001-570621/64.	974	GAGCTGTGTCAGCGGATCACGACGAGCAGGAGGAGGAGGCTTTCATCGAGGCTCTG	1033
DR	P-PSDB; AAG63832.	970	GAGCTGTGTCAGCGGCTGGCCCGGAGCAAGAGGAGAGCTCGAGCGCTCCGCGGCTC	1029
XX	Nucleic acid encoding a cardiomyopathy associated protein that is	1034	ATCTCTCAGTACAGGAGCAGCTGGAAGAGTCCCAAGCTTTGTGAGAGACCGCCATCCAG	1093
PT	differentially expressed in human left ventricle assist device (LVAD)	1030	ATCCGTTCAGTATGCGACCACTGCGAGGCTCTCTAAGCTGGTGGAGTCTGCCATCCAG	1089
PT	myocardial biopsy samples, useful for diagnosing, preventing or treating	1094	TCCCTGGATGAGCCGCGAGGGCTACCTTCTCAAGTGCACAGCAGCTCATCAAGAGC	1153
XX	cardiomyopathy.	1090	TCCATGGAAGAGCCACAATGGCGTGTATCTCCAGCAGGCGCAGGAGTGAATCAATAG	1149
PS	Claim 2; Page 49-51; 55pp; English.	1154	ATTGTAGAAGCTCTCAAGGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTTGAGAACATG	1213
CC	The present sequence encodes a human cardiomyopathy associated protein	1150	GTCGGGCGCATGTCGAGGTGGAGTGGCAGGGCGCGGAGCCAGGCTATGAGAGCATG	1209
CC	(CAP) that is differentially expressed in human left ventricle assist	1214	GACTACTTTTACTCTGGAGCTTAGAACATAGCAGAGGCTTTGAGGCGCATGACTTTGGG	1273
CC	device (LVAD) myocardial biopsy samples. The predicted isoelectric point	1210	GAGCAATTCACCGTAAGGGTGGAGCAGCTGGCCGGAATGCTCGGAGCATCGACTTCCAG	1269
CC	of CAP is approximately 12.2. The CAP polynucleotide and polypeptide are	1274	ACAGG 1278	
CC	useful for diagnosing, preventing or treating cardiomyopathy. The	1270	CCAGG 1274	
CC	treatment diminishes the occurrence of at least one of the following			
CC	symptoms associated with cardiomyopathy: reduced ejection fraction,			
CC	increased left ventricular diastolic dimension, decreased ventricular			
CC	wall thickness, increased atrial size, valvular regurgitation, exertional			
CC	intolerance or ventricular tachyarrhythmia. Modulators of CAP are also			
CC	useful for preventing or treating cardiomyopathy			
XX	Sequence 1990 BP; 524 A; 535 C; 613 G; 318 T; 0 U; 0 Other;			
SQ				
	Query Match			
	Best Local Similarity 30.2%; Score 481.8; DB 4; Length 1990;			
	Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;			
QY	317 CTGATTCCTGATGGAACCGCTATGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTGCG	376		
Db	310 CTGCTAGGGATGACACAGCATGACCACTGGAGAGCAGCTCATCTGCCCATCTGCG	369		
QY	377 CTGAGATGTTTACCAAGCTGTGTCTATCTCTGCTGCTGCAACACATCTGCGGAG	436		
Db	370 CTGAGATGTTTCTCAACACAGTGTGTCTCTGCTGCTGCAACACATCTGCGGAG	429		
QY	437 TGTGCAACGACATCTTCAGGCTGCGAATCCTACTTGACCAACCGGCTGCTGAGTG	496		
Db	430 TGTGCAACGACATCTTCAGGCTGCGAATCCTACTTGACCAACCGGCTGCTGAGTG	489		
QY	497 TCCATGCTCGAGGTGCTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	556		
Db	490 GTGCTCTCAGGAGGCGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	549		
QY	557 CACGGGTGTACGGCTGACAGGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	616		
Db	550 CACGGGTGTACGGCTGACAGGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	609		
QY	617 CAGGAGTGTCCAG--TCGGCCCTGACAGGAGCAGCCACCGATGTGCAAGAACAC	673		
Db	610 CAGGAGTGTATCAGGCGCTGACCTCAAGGCTGAGCAGCAGCTCATGTGCGAGGAGAT	669		
QY	674 GAAGCAGAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCTGCTGCTGCTGCTG	733		
Db	670 GAAGCAGAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCTGCTGCTGCTGCTG	729		
QY	734 AAGGTGTTGGGGCTCACCAGGCTGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTG	793		
Db	730 AAGGTGTTGGGGCTCACCAGGCTGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTG	789		
QY	794 CAGAAGAGTGTGCTGAGTAACTGCAATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTG	853		
Db	790 CAGAAGAGTGTGCTGAGTAACTGCAATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTG	849		
QY	854 ACATCATCTCTCAGCTGAGGAGCTGCTGAGGAGTGAACCAAGAGATAGCCACAGGTG	913		
Db	850 GCAGTGTATCACACAGATGAGGAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	909		
QY	914 AAGGAGGAGTGTGCTGAGAGTTTGCACACCTCTTACGCTGCTGCTGCTGCTGCTG	973		

RESULT 19

AAA72433

ID AAA72433 standard; cDNA; 1349 BP.

AC AAA72433;

DT 19-DEC-2000 (first entry)

XX Human nucleic acid-binding protein NuABP-52 cDNA.

DE Human nucleic acid-binding protein; NuABP; agonist; antagonist; EST;

XX expressed sequence tag; drug screening; recombinant expression; antibody;

KW reproductive disorder; infertility; immunological disorder;

KW neurological disorder; cell proliferative disorder; cancer; tumour; ss.

XX Homo sapiens.

XX WO20044900-A2.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US002237.

XX 29-JAN-1999; 99US-0117904P.

XX 29-JAN-1999; 99US-0117905P.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Yue H, Azimzai Y, Lu AMD, Baughn MR;

XX Tran B, Shih LL, Au-Young JL;

XX WPI; 2000-499332/44.

XX P-PSDB; AAB21048.

XX Novel nucleic acid binding proteins, used to identify agonists and

PT antagonists of them, for the treatment of reproductive, immunological,

PT neurological and cell proliferative disorders including cancer.

XX Claim 4; Page 178-179; 180pp; English.

XX Sequences AAA72382-A72436 represent cDNAs encoding novel human nucleic

CC acid-binding proteins (NuABPs; AAB20997-B21051). These cDNAs were

CC produced by extension from an appropriate EST (expressed sequence tag)

CC using primers designed using the EST. The invention also relates to

CC expression constructs, host cells and transgenic organisms comprising a

CC human NuABP nucleic acid, recombinant production of the human NuABPs, and



CC toxins or drugs. The MURF1, MURF3 and MAFBX antagonists, and the  
CC antagonists of their pathways are useful for inhibiting atrophy, inducing  
CC hypertrophy, decreasing ubiquitination, interfering with the ubiquitin  
CC pathway, or modulating MURF1, MURF3 or MAFBX expression or activity. The  
CC nucleotide sequences are useful for diagnostic and genetic testing. The  
CC present sequence represents a human MAFBX protein encoding DNA  
XX  
SQ Sequence 867 BP; 204 A; 242 C; 258 G; 163 T; 0 U; 0 Other;

Query Match 27.8%; Score 444.4; DB 6; Length 867;  
Best Local Similarity 71.5%; Pred. No. 6e-108;  
Matches 599; Conservative 0; Mismatches 236; Indels 3; Gaps 1;

QY 317 CTGATTCTCTGATGGAACGCTATGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTGC 376  
DB |||||  
QY 377 CTGGAGATGTTTACCAAGCTGTGTCTATCTCCCTGCTGCAACACAACTCTGCCGGAAG 436  
DB |||||  
QY 88 CTGGAGATGTTTCTCAAAACCACTGTGTGATCTCTGCCCTGCCAACACAACTGTGCCGCAA 147  
DB |||||  
QY 437 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCTCAGTG 496  
DB |||||  
QY 148 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCTCAGTG 207  
DB |||||  
QY 497 TCCATGTCTGGAGGTGTTTCCGTTGCCCTCGTCCGCCATGAAGTGAATCATGGACCGG 556  
DB |||||  
QY 208 GTGTCTTCAGGAGGCGGTTTCGCTGCCCATCGTCAGGCGATGAGTTGTCTCGACAGA 267  
DB |||||  
QY 557 CACGGGGTGTACGGCTGACAGAGAACCTGCTGGTGGAAACATCATTTGACATCTACAAG 616  
DB |||||  
QY 268 CACGGTGTCTACGGCTGACAGAGAACCTGCTAGTGGAGAACATTTATGACATTTACAAG 327  
DB |||||  
QY 617 CAGGAGTGTCTCAG--TCGGCCCTGCAGAAAGCAGCCACCGATGTGCAAGGAACAC 673  
DB |||||  
QY 328 CAGGAGTGTATCAGGCGCTGCACTCCAGGCTGAGCAGCACCTCATGTGCGAGGAGCAT 387  
DB |||||  
QY 674 GAAGACGAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCTTACTTGTCTTGTGC 733  
DB |||||  
QY 388 GAAGAAGAGAGATCAATATTTACTGCTGAGCTGTGAGGTGCCACCTGTCTCTCTGC 447  
DB |||||  
QY 734 AAGGTGTTTGGGGCTCACAGGCTGTGAGGTGCTTGTGCAAGCATCTTCCAAGGA 793  
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QY 448 AAGGTCTTCGGTGGCCACAGGACTGTGAGGTGGGCCCACTGCCACCATTTACAACGC 507  
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QY 794 CAGAGACTGAGCTGAGTAACCTGCTATCTCTGCTGGTGGGGGAAACGACCGAGTGCAG 853  
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QY 508 CAGAGAGTGAAGCTCAGCGATGGCATCGCGATGCTGTGGCAGGCAATGACCGCGTGCAA 567  
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QY 854 ACGATCATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAATAGCCACAGGTG 913  
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QY 568 GCAGTGATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACAAATAGCCGAGGCAG 627  
DB |||||  
QY 914 AAGGAGGAGCTGAGTCAAGTTTGCACCCCTCTAGCCATCTCGATGAGAGAGAGCAGC 973  
DB |||||  
QY 628 AAGCAGTTGTTAAACCCAGAGGTTTGAAGGCTGTGCGCAGTGTGCGAGGAGCGCAAGG 687  
DB |||||  
QY 974 GAGCTGCTCAGCGGATCACGAGGAGGAGGAGGAGTGGGCTTCATCGAGGCTCTG 1033  
DB |||||  
QY 688 GAGCTGCTCAGCGGCTGCGCGGAGGAGGAGGAGGAGTGGGCTTCATCGAGGCTCTG 747  
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QY 1034 ATCTCTCAGTACAGGAGCAGCTGGAAGAGTCCACCAAGCTTGTGGAGACCGCCATCCAG 1093  
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QY 1094 TCCCTGGATGAGCCGGAGGGGCTACCTTCCTCTCAAGTGCCAGCAGCTCATCAAGA 1151  
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QY 808 TCCATGGAAGAGCCCAAAATGGCGTGTATCTCCAGAGGCCCAAGAGCTGATCAATA 865  
DB |||||





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OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:37:10 ; Search time 4801 Seconds  
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12661.662 Million cell updates/sec

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Perfect score: 1597

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	576.8	36.1	769	CO560583	AGENCYCOURT
3	563	35.3	912	BI758535	603022861
4	554.6	34.7	655	CA333888	NISC_1803
5	546.2	34.2	868	BG764060	602737069
6	539.6	33.8	1105	BG761218	602718564
7	538.6	33.7	793	BI754358	603026906
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9	505.6	31.7	1142	BU470941	603363447
10	497.8	31.2	952	BU241018	603323733
11	496.6	31.1	682	BG769996	602745109
12	496.2	31.1	966	BU135007	603119195
13	481.8	30.2	1077	AY411684	Homo sapi
14	478.4	30.0	991	AY411685	Pan trogl
15	477.8	29.9	890	BU107891	603111441
16	474.4	29.7	1083	AY411686	Mus muscu
17	472.8	29.6	803	CK128385	AGENCYCOURT
18	460.2	28.8	835	BU438107	603209639
19	457.4	28.6	464	AI644642	vw79b06.x
20	441	27.6	731	CN037969	nm 25 bl7
21	421	26.4	996	BU385902	603581640
22	412.2	25.8	801	BU452003	603216327
23	411.6	25.8	465	2	BB857510
24	411.2	25.7	633	7	CR767305

CR767305 DKF2p468L

25	394.4	24.7	800	5	BU220426	603756441
26	389.4	24.4	497	5	EX283938	EX283938
27	381.6	23.9	490	2	AW296154	UI-H-B12-
28	379.2	23.7	1455	3	CR677834	Tetraodon
29	373.2	23.4	1466	3	CR670382	Tetraodon
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31	361.8	22.7	852	5	BU382730	603583583
32	359.6	22.5	561	5	BP259752	BP259752
33	359.2	22.5	775	7	CF290486	AGENCYCOURT
34	358.4	22.4	786	7	CF289491	AGENCYCOURT
35	357.4	22.4	554	5	BP259119	BP259119
36	355	22.2	530	6	CD215266	pgm2n.pk0
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41	341.8	21.4	543	5	BX500821	DKF2p779G
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43	335	21.0	699	5	BU385958	60358544
44	333.4	20.9	449	6	CB742808	AMGNNUC:N
45	329.8	20.7	822	5	EX427830	EX427830

ALIGNMENTS

RESULT 1  
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LOCUS CK603034 807 bp mRNA linear EST 22-JAN-2004  
DEFINITION AGENCYCOURT\_17899884 NIH\_MGC\_234 Rattus norvegicus cDNA clone  
IMAGE:7193197 5', mRNA sequence.  
ACCESSION CK603034  
VERSION CK603034.1 GI:41116353  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 807)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Howard Jacobs  
cDNA Library Preparation: Express Genomics  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM15055 row: b column: 11  
High quality sequence stop: 643.  
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/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_234"  
/note="Organ: heart; Vector: pExpress-1; Site: 1: EcorV;  
Site 2: NotI; RNA obtained from pooled heart tissue from a  
mix of male and female animals at 8 wk old. Tissues were  
snap-frozen and kept at -80C for two days before RNA  
extraction and purification (Tri-reagent method). cDNA was  
primed using oligo-dr primer:  
5'-pgactagtttagatcgagcgccccc(T)25-3' and cloned into

FEATURES  
source

the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH\_MGC\_233) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH\_MGC library."

ORIGIN	
Query Match	38.3%; Score 611.2; DB 7; Length 807;
Best Local Similarity	92.7%; Pred. No. 1.1e-150;
Matches 674; Conservative	0; Mismatches 49; Indels 4; Gaps 3;
QY	259 TGTGACGCGAGGTGGGCAAGACAGTCGCA-TTTCAAAGCAATATGGATTATAAATCTAGCC 317
Db	1 TGTGACGCGAGGTGGAAGAGACAGTCGCGAGTTTCGAAGCAATATGGATTATAAATCTGGCT 60
QY	318 TGNATTCTCATGGAAGCGCTATGGAGAACTGGAGAGCAGCTGATCTGCCCATCTGCC 377
Db	61 TGNATCCGACGGAATGCTATGGAGAACTGGAGAGCAGCTCATCTGCCCATCTGCC 120
QY	378 TGGAGATGTTTACCAAGCGCTGTGGTCATCTGCGCTGCCAACACACACCTCTGCGGAAGT 437
Db	121 TTGAGATGTTTACCAAGCGCTGTGGTCATCTGCGCTGCCAACACACCTCTGCGGAAGT 180
QY	438 GTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGCCAAACCCGGTGGCTCAAGT 497
Db	181 GTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGCCAAACCCGGTGGCTCAAGT 240
QY	498 CCATGCTCGGAGTCTGTTCCGTCGTCCTCGTCCGCCCATGAGTGATCGACCGGC 557
Db	241 CCATGCTCGGAGTCTGTTCCGTCGTCCTCGTCCGCCCATGAGTGATCGACCGGC 300
QY	558 ACGGGGTGTACGGCTCGCAGAGAACTGCTGTGTGAAAACATCATTTGACATCTACAAGC 617
Db	301 ATGGGGGTGTACGGCTGTGAGAGAACTGCTGTGTGAAAACATCATTCGACATCTACAAGC 360
QY	618 AGAGTGTCTCCAGTCGGCCCTGSCAGAAAGGCGACCCCGATGTGCAAGGAACACGAAG 677
Db	361 AGGAATGCTCCAGTCGGCCCTGSCAGAAAGGCGACCCCGATGTGCAAGGAACACGAAG 420
QY	678 ACGAGAGATCAACATCTACTGTCTACGTTGAGGTGCTACTTCTCTTGTGCAAGG 737
Db	421 ACGAGAAATCAACATCTACTGTCTACGTTGAGGTGCTACTTCTCTTGTGCAAGG 480
QY	738 TGTTCGGGCTCACAGGGCTGTGAGGTTGCCCCCTTTGCAAGCATCTTCCAGGACAGA 797
Db	481 TGTTCGGGCTCACAGGGCTGTGAGGTTGCCCCCTTACAGAGCATCTTCCAGGACAGA 540
QY	798 AGACTGAGCTGAGTAATCTGATCTCCATGCTGTGTGGCGGGGAACGACCGAGTGCAGCA 857
Db	541 AGACTGAACTGAGCAATGTCATCTCCATGCTGTGTGGCGGGGAACGACCGAGTTCAGACTA 600
QY	858 TCATCTCTCAGCTGGAGGACTCGTCAGAGTGACCAAGGAGATAGCCACCGAGTGAAGG 917
Db	601 TCATCTCGCAGCTGGAGGACTCGTCGAGTGACCAAGGAAACAGCCACCGAGTGAAGG 660
QY	918 AGGAGCTGAGTCAGAAATTTGACACCTCTACGCCATCTCGGATGAGAAAGAGCGAGC 977
Db	661 AGGAATGAGCCA-CACTTTGAGCCCTCTACGCCATCTGGA--CAGAGAGAGTGAAGC 717
QY	978 TGCTGCA 984
Db	718 TGCTGCA 724

RESULT 2  
COS60583  
LOCUS  
DEFINITION  
AGENCOURT 28621713 NIH MGC 250 Rattus norvegicus cDNA clone  
IMAGE:7383160 5', mRNA sequence.  
ACCESSION  
COS60583  
VERSION  
COS60583.1 GI:50373179  
KEYWORDS  
EST.  
Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE

1 (bases 1 to 769)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

AUTHORS

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Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

JOURNAL

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
College of Wisconsin

COMMENT

CDNA Library Preparation: Open Biosystems  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

FEATURES

Plate: LAM1546 row: a column: 14  
High quality sequence stop: 683.

source

Location/Qualifiers  
1..769

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clone="IMAGE:7383160"

/lab\_host="DH10B TonA"

/clone\_lib="NIH MGC 250"

/note="Organ: thymus; Vector: pExpress-1; Site 1: EcorV;  
Site 2: NotI; RNA obtained from testis tissue of 8 wk old  
animal. Tissues were snap-frozen and kept at -80C before  
RNA extraction and purification (Tri-reagent method). cDNA  
was primed using oligo-dT primer:  
5'-pGACTAGTCTAGATCGCGAGCGGCC(T)25-3' and cloned into  
the EcorV/NotI sites of pExpress-1. Size-selection >1.25kb  
resulted in an average insert size of 1.9 kb. This is a  
primary library (normalized library is NIH\_MGC\_251) and  
was constructed by Open Biosystems. Note: this is a  
NIH\_MGC library"

ORIGIN

Query Match 36.1%; Score 576.8; DB 7; Length 769;  
Best Local Similarity 94.1%; Pred. No. 1.4e-141;  
Matches 610; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY	253 ACTTGGTGTGACGCGAGGTGGCAAGACAGTCGCA-TTTCAAAGCAATATGGATTATAAAT 311
Db	34 ACTCGGTGTGACGCGAGGTGGAAGAGACAGTCGCAGTTTCGAAGCAATATGGATTATAAAT 93
QY	312 CTAGCCCTGATTTCTGATGGAAAACGCTATGGAGAACTGGAGAGCGAGCTGATCTGCCCA 371
Db	94 CTGGCTTGATTCCGACCGGAAATGCTATGGAGAACTGGAGAGCGAGCTCATCTGCCCA 153
QY	372 TCTGCTCGGAGATGTTTACCAAGCGCTGTGTCATCTCTGCCCTGCCAACACCACTCTGCC 431
Db	154 TCTGCTTGGAGTGTTTACCAAGCGCTGTGTCATCTCTGCCCTGCCAGCAACCTCTGCC 213
QY	432 GGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCT 491
Db	214 GGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCT 273
QY	492 CAGTGTCCATGTCTGAGGTCTGTTCCGTTGCCCTCTGTCGCCCATGAAGTGATCATGG 551
Db	274 CGGTGTCCATGTCTGAGGTCTGTTCCGCTGCCCTCTGTCGCCCATGAAGTGATCATGG 333
QY	552 ACCGCGACGGGTGTACGCGCTCGAGAGAACTGCTGTTGGAAAACATCATTTGACATCT 611
Db	334 ACCGGCATGGGTGTACGCTCTGAGAGAACTGCTGTTGGAGAAACATCATCGACATCT 393
QY	612 ACAAGCAGGAGTGTCTCAGTCCGCCCTCTGCAGAAAGGCGACCCCGATGTGCAAGAAC 671



DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
Plate: LLAM12387 row: D column: 17  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. .655  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:5599072"  
/sex="male"  
/tissue type="dorsolateral prostate, pool of 3-, 5-, and 7-days post-castration"  
/dev\_stage="adult, 11 week"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP Pr50"  
/notes="Organ: prostate; Vector: pCMV-SPORT6.1; Site 1: Not1; Site 2: EcoRV; Cloned unidirectionally. Primer: Oligo dt. Pool of 3 primary libraries: NCI\_CGAP\_Pr39 (dorsolateral prostate from 11 wk male, 3 days post-castration, average insert size 2.7 kb), NCI\_CGAP\_Pr29 (dorsolateral prostate from 11 wk male, 5 days post-castration, average insert size 2.2 kb) and NCI\_CGAP\_Pr42 (dorsolateral prostate from 11 wk male, 7 days post-castration, average insert size 2.2 kb). This is constructed by Life Technologies/Invitrogen. Note: this is a NCI\_CGAP Library."

FEATURES  
source

ORIGIN

Query Match 34.7%; Score 554.6; DB 6; Length 655;  
Best Local Similarity 94.4%; Pred. No. 1.1e-135;  
Matches 586; Conservative 0; Mismatches 34; Indels 1; Gaps 1;  
  
QY 253 ACTTGCTGTGACGAGTGGCGAAGACAGTCGCA-TTTCAAAGCAATATGGATTATAAAT 311  
DB 35 ACTCGGTGTGACGAGTGGGAAGACAGTCGCGAGTTTCGAGCAATATGGATTATAAAT 94  
  
QY 312 CTAGCCCTGATTCTGTATGNAACGCTATGGAGAACCTGGAGAGAGAGCTGATCTGCCCA 371  
DB 95 CTGGCTTGATTCCGCGACGGAATGCTATGGAGAACCTGGAGAGAGAGCTCATCTGCCCA 154  
  
QY 372 TCTGCTCGGAGATGTTTACCAAGCCTGTGTCTATCTGCCCTGCCCAACAACTCTGCG 431  
DB 155 TCTGCTCTGAGATGTTTACCAAGCCTGTGTCTATCTGCCCTGCCCAACAACTCTGCG 214  
  
QY 432 GGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGTGGCT 491  
DB 215 GGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGTGGCT 274  
  
QY 492 CAGTGTCCATGCTGAGAGTGTGTTTCCGCTGCCCTCGTGCCTGCGCCCATGAAGTATCATGG 551  
DB 275 CGGTGTCCATGCTGAGAGTGTGTTTCCGCTGCCCTCGTGCCTGCGCCCATGAAGTATCATGG 334  
  
QY 552 ACCGCGACGGGTGACGGCTCCAGAGGAACCTGCTGGTGGGAAAACATCATTTGACATCT 611  
DB 335 ACCGCGATGGGGTGTACGGTCTCCAGAGGAACCTGCTGGTGGGAAAACATCATTCGACATCT 394  
  
QY 612 ACAAGCAGGAGTGCTCCAGCTCGGCCCTCGCAGAAAGCGACCAACCGCATGTGCAAGGAAC 671  
DB 395 ACAAGCAGGAATGCTCCAGTCCGCCCTCGCAGAAAGCGACCAACCGCATGTGCAAGGAAC 454  
  
QY 672 ACAGAGCAGGAAGATCAACATCTACTGTCTACAGTGTGAGGTGCGCTACTTGTCTCTTGT 731  
DB 455 ACAGAGCAGGAATAATCAACATCTACTGTCTCAAGTGTGAGGTGCGCTACTTGTCTCTTGT 514  
  
QY 732 GCAAGGTGTTTGGGGTTCACAGGCTGTGAGGTGCGCCCTTTGCAAAAGCATCTTCCAAG 791  
DB 515 GCAAGGTGTTGGGGTTCACAGGCTGTGAGGTGCGCCCTTTACAAAGCATCTTCCAAG 574  
  
QY 792 GACAGAAGACTGAGCTAGTAATCTGCATCTCCATCTGCTGTGGCGGGAAACGACCGAGTGC 851

DB 575 GACAGAAGACTGAACCTAGCAATTCATCTCCATGCTGCTGGCAGGAACACCGAGTTC 634  
QY 852 AGACGATCATCTCTCAGCTGG 872  
DB 635 AGACTATCATCTCGCAGCTGG 655  
  
RESULT 5  
LOCUS BG764060 868 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602737069F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4862321 5', mRNA sequence.  
ACCESSION BG764060  
VERSION BG764060.1 GI:14074713  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
MAMMALIA; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 868)  
NIH-MGC http://mgs.nci.nih.gov/.  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC) UNPUBLISHED (1999)  
CONTACT: Robert Strausberg, Ph.D.  
EMAIL: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/BTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLCM1722 row: j column: 18  
High quality sequence stop: 863.  
  
FEATURES  
source  
1. .868  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4862321"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 49"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. |"  
  
ORIGIN  
  
Query Match 34.2%; Score 546.2; DB 4; Length 868;  
Best Local Similarity 85.0%; Pred. No. 2e-133;  
Matches 669; Conservative 0; Mismatches 113; Indels 5; Gaps 5;  
  
QY 262 GACGACGTTGGGCAAGACAGTCGATTCCTCAAGCAATATGGATTATAATCTAGCTGAT 321  
DB 83 GAGGACGCTAGCGTGGCTCTCTATTCTCCCAAGATGGATTATAAGTCGAGCTGAT 142  
  
QY 322 TCCTGATGAAACCGCTATGGAGAACCTGGAGAGCAGCTGATCGCCCATCTGCCCTGGA 381  
DB 143 CCAGGATGGAAATCCCAAGAACCTGGAGAGCAGCTGATCGCCCATCTGCCCTGGA 202  
  
QY 382 GATGTTTACCAAGCCCTGTGTCTCATCTGCGCTGCCCAACCAACCTCTGCCGAAGTGTGC 441  
DB 203 GATGTTTACCAAGCCAGTGTGTCTCTTGGCGTGGCAGCACACCTGTGCGGAAGTGTGC 262  
  
QY 442 CAAACGACATCTTCCAGGCTGCGAATCCCTACTGTGGAACCAACCGCGGTGGCTCAGTGTCCAT 501





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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4869740"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_49"
/notes="Organ: Skin; Vector: pOT97; Site1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Size-selected ~500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Bscript II RT (Life Technologies). Note: this is a NIH MGC Library."

```

## ORIGIN

```
Query Match      32.5%; Score 519; DB 4; Length 721;
Best Local Similarity 86.4%; Pred. No. 3.1e-126;
Matches 573; Conservative 0; Mismatches 90; Indels 0; Gaps 0
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Qy	630	GTGGGCCCTGCGAAGAGCGAGGCCACCCGATGTGCAAGGAACACGAAGCAGAGAGATCA	689
Dd	2	GTGGCCGCTGCGAAGAGGCGAGTCACCCCATGTGCAAGAGAGCACGAAGATGAGAAAATCA	61

Qy	690	ACATCTACTGTCTCACGTTGAGGTGCCCTTGTCTCTTGTGCAAGTGTGTTGGGGCTC	749
Db	62	ACATCTACTGTCTCACGTTGAGGTGCCCACTGTCTCCATGTGCAAGTGTGTTGGGATCC	121

Qy	750	ACCAGGCGCTGTGAGGTTGGCCCTTTGCAAGGCACTCTTCAAGGACAGAGACTGAGCTGA	809
Db	122	ACAAGGCTCGGAGGTGGCCCATTCGACAGTGCTTTCAGGGGACAAAGACTCGAACTGA	181

Qy	810	GTAACTGCAATCTCCATGCTGGTGGCGGGGAAACGACCGAGTGGCAGACGATCATCTCTCAGC	869
D <sub>b</sub>	182	ATAACTGTGATCTCCATGCTGGTGGCGGGGAAATGACCGGTGGCAGACCATCATCACTCAGC	241

Qy	870	TTGAGGACTTCGTGCAGAGTGCACCAAGGAGNAATGCCACCAAGGTGNAAGGAGGAGCTTGAGTC	929
Db	242	TGAGAGGATTCCTCCGTCGAGTGCACCAAGGAGAACAGTCACCAAGGTAAAGGAAAGAGCTTGAGCC	301

Qy	930	AGAAAGTTTGACACCCCTCTACGCCATCTCGGATGAGAAAGAGCGGAGCTGCTGCAGCGGA	989
Db	302	AGAAAGTTTGACACGTTGTATGCCATCTCGGATGAGAAAGAGTGAGTTCTGTCAGCGGA	361

Qy	990	TCACGCAGGACGAGGAGAACTGGGCTTCATCGAGGCTCTGATCTCTCCAGTACAGGG	104
Db	362	TCACGCAGGACGAGGAGAAAGCTTAGCTTCGAGGGCCCTCATCCAGCAGTACCAAGG	421

Qy	1050	AGCAGCTGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTCGATGAGCCCG	1108
Db	422	AGCAGCTGGAACAAGTCCACAAAGCTGGTGAACCTGCCATCCAGTCCCTCGACGAGCCTG	481

Qy	1110	GAGGGGTCACCTTCTCTCAAGTGCACGAGCTCATCAAGAGCATTTGTGAAGGCTCCA	1161
Db	482	GGGGAGCCACCTTCTCTTGACTGCGAAGCACTCATCAAAAGCATTTGTGGAAGCTCCCA	541

Qy	1170	AGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAA	CATGCACTACTTTTACTCTGG	122
Db	542	AGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAA	CATGCACTTTTACTTTGG	601

Qy	1230	ACTTAGAACACATAGCAGAGGCCCTTGGAGGCCATTGACTTTTGGGACAGGTAAGGATGTG	128
Db	602	ATTTAGAGCACATAGCAGACGCCCTTGAGGCCATTGACTTTTGGGACAGATGAGGAAGAGG	661

Qy	1290	ATG	1292
D <sub>b</sub>	662	AAG	664

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VERSION	BU470941.1
KEYWORDS	GI:25964518
SOURCE	EST.
ORGANISM	Gallus gallus (chicken)
REFERENCE	Gallus gallus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
TITLE	1 (bases 1 to 1142)
JOURNAL	Boardman,P.E., Sanz-Esquerro,J.J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
MEDLINE	A Comprehensive Collection of Chicken CDNAs
PUBMED	Curr. Biol. 12 (22), 1965-1969 (2002)
COMMENT	12445392
	Contact: Simon Hubbard
	Department of Biomolecular Sciences
	University of Manchester Institute of Science and Technology
	(UMIST)
	PO Box 88, Manchester, M60 1QD, UK
	Tel: 01612008930
	Fax: 01612360409
	Email: Simon.Hubbard@umist.ac.uk.

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/notes="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

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## ORIGIN

	Query Match	31.7%	Score 505.6;	DB 5;	Length 1142;
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	Matches 687;	Conservative 0;	Mismatches 224;	Indels 7;	Gaps 4;
Qy	299	ATGGATTATATAAATCTAGCCCTGATTCTCTGATGGAGAAACGCTATGGAGAACCTCGGAGAACGAG	358		
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Qy	359	CTGATCTGCCGCCCATCTGCCCTGGAGATGTTTACCAAGCCTGTGTCTATCCTGCCCTGCCAA	418		
Db	120	CTGCTGTGCCCCCATCTGCTCTGGAGATGTTTCAGCAAGCCTGTGTGTGATCTCTGCCCTCGCAA	179		
Qy	419	CACAACTCTTCGCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCTCTACTCGACC	478		
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Qy	479	AACGGCGGTGGCTCAGTGTCCATGTCTGGAGGTGGTTCCGTTGCCCTCGTCCGCCCAT	538		
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RESULT 9  
BU470941  
LOCUS

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VERSION BU241018.1 GI:25487197  
KEYWORDS EST.  
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ORGANISM Gallus gallus  
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1 (bases 1 to 952)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392  
PUBMED  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
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/note="Organ: liver; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

FEATURES  
source

ORIGIN

Query Match 31.2%; Score 497.8; DB 5; Length 952;  
Best Local Similarity 75.5%; Pred. No. 1.4e-120;  
Matches 657; Conservative 0; Mismatches 208; Indels 5; Gaps 3;

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Db 63 GCAGGAGCAT---CATCTCGGAGGCGGTTCCGCTGCTCCCTACGTGCCGCCACGAGTCC 119  
Qy 546 TCATGACCGGCACCGGGGTGTACGGCTGCAGAGAACTCTGTGTGGAAAAACATCATTTG 605  
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Qy 606 ACATCTACAGCAGAGAGTCTCAGTGGCCCTCGAGAAAGGAGCAGCCAGCATGTGCA 665  
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Qy	1146	-TCAAGAGCATTTGTAAGGCTCCCAAGGGCTGCCAGCTGGGGAAGACAGAGCAAGGGCTTT	1204
Db	719	TTTAAACGATTTGTAAGGCTCCAGGGCGGCGAGGCTGGAGAAGATTGAGCAAGGCTAT	778
Qy	1205	GAGAACAATGGACTACTTTTACTCTGGACTTAGAACAACATAGCAGAGGGCTTTGAGGGCCATT	1264
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DEFINITION			
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BG769996			
VERSION			
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SOURCE			
ORGANISM			
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 682)			
NIH-MGC http://mgc.nci.nih.gov/.			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-r@mail.nih.gov			
Tissue Procurement: ATCC/DCTP/DRP			
CDNA Library Preparation: Ling Hong/Rubin Laboratory			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
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1.8kb. Library constructed by Ling Hong in the laboratory			
of Gerald M. Rubin (University of California, Berkeley)			
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II RT (Life Technologies). Note: this is a NIH_MGC			
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85.7%; Pred. No. 2.7e-120;			
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2; Gaps			
2;			

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

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QY 419 CACAACTCTGCCGGAAGTGTGCAACGACATCTTCAGGCTCGGAATCCTACTCGACC 478  
DB 159 CACAACTCTGCCGGAAGTGTGCAACGACATCTTCAGGCTCGGAATCCTACTCGACC 218  
QY 479 AACCGGTGTGCTAGTGTCATGTCTGGAGTGTGTTCCGTTGCCCTCGTGCCTCCAT 538  
DB 219 AGCCGAGGAGCAGCAT--CATCTCGGAGGCGGTTCGCTGCCCTACGTGCGGCCAC 275  
QY 539 GAAGTGTATGATGACCGGACGGGTGTACGGCTCGAGGAACTCTGCTGTGGAAAC 598  
DB 276 GAGTCTCTGTGACCGCCACGGTGTCTATGGGCTGCAAGGAACCTGCTGTGGAGAAC 335  
QY 599 ATCATTTGACATCTACAGCAGGAGTGTCTCAGTCCGCGCCCTGCAAGAAAGCAGCCCG 658  
DB 336 ATCATCGACATCTACAGCAGGAGTGTCTCAGCAGGCGCACTCAAGAGGGGAGCACCC 395  
QY 659 ATGTCAAGAAACCAAGACGAGAGATCAACATCTACTGTCTACGTGTGAGTGGCT 718  
DB 396 ATGTCAAGAGGATGATGAGGACGAGCGATCAACATCTACTGTCTACGTGCGAGTCCC 455  
QY 719 ACTTGCTCTGTGCAAGTGTGTGGGCTCACCAGCCTGTGAGTGTGCCCTTTGCA 778  
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REFERENCE 1 (bases 1 to 1077)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1077)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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18	484.6	30.3	1431	6	AX418848 Sequence
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20	482.4	30.2	1270	5	BX934363	BX934363 Gallus ga
21	481.8	30.2	1077	6	CQ721328	CQ721328 Sequence
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ALIGNMENTS

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DEFINITION Sequence 5 from Patent WO0206318.  
ACCESSION AX418852  
VERSION AX418852.1 GI:21523716  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Olson,E.N. and Spencer,J.A.  
TITLE Methods and compositions for stabilizing microtubules and intermediate filaments in striated muscle cells  
JOURNAL Patent: WO 0206318-A 5 24-JAN-2002;  
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)  
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CDS

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Query Match 100.0%; Score 1597; DB 6; Length 1597;  
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1 CTCGAGATTACCTTACAGAGCTGTTCGGAGGACCTTTCCTTGGCAGCACACTCAG 60  
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Qy	121	GCAGACCATGGATAACTTTGGAAAGCAACTGTCTGTCCCATCTGCTCCTAGAGATGTTTAC	180
Db	121	GCAGACCATGGATAACTTTGGAAAGCAACTGTCTGTCCCATCTGCTCCTAGAGATGTTTAC	180
Qy	181	GAAGCCTGTGGTCATTTCTCCCTTGCAGCAACAACCTGTGTGCAGGAATGTGCGGGCCCCC	240
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LOCUS	MGC:72330	IMAGE:599072	complete cds.	
DEFINITION	BC061824	GI:38197349		
ACCESSION	BC061824			
VERSION	BC061824.1			
KEYWORDS	MGC.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
REFERENCE	1 (bases 1 to 1858)			
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
PUBMED	12477932			
REFERENCE	2 (bases 1 to 1858)			
AUTHORS	Strausberg,R.			
TITLE	Direct Submission			

## JOURNAL

Submitted (05-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Magliello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, J.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 137 Row: 9 Column: 8  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18266713.

FEATURES  
source

Location/Qualifiers

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NCI CGAP\_Pr29, 39, 42"

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Best Local Similarity 93.1%; Pred No. 2.9e-203;

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Db 95 CTGGCTTGAATTCGCGACGGAATGCTATGGAAACCTGGAGAAGCAGCTCATCTGCCCA 154

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Db 1055 GGACAGGTAAAGGATGTGATGTTAC 1079

## RESULT 3

AY059627

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

AY059627 1861 bp mRNA linear ROD 13-DEC-2001  
Rattus norvegicus muscle ring finger protein 1 mRNA, complete cds.

AY059627.1 GI:16444655



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DB 1419 GGAAGAGGAG 1429

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LOCUS Human mRNA for muscle specific RING finger 2 (MURF2) protein (MURF2  
gene).

ACCESSION AJ276484  
VERSION AJ276484.1 GI:18073355  
KEYWORDS MURF2 protein; RING finger protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1756)  
AUTHORS Stanchi, F.  
TITLE Characterisation of MURF2, a new muscle-specific RING finger  
protein of the RBCC family that associates with microtubules  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1756)  
AUTHORS Stanchi, F.  
TITLE Direct Submission  
JOURNAL Submitted (20-MAR-2000) Stanchi F., CRIBI Biotechnology Centre,  
Universita di Padova, Via G. Colombo 3, Padova, 35121, ITALY

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gene  
exon  
CDS





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RESULT 7

BC080529

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC080529 1764 bp mRNA linear PRI 30-AUG-2004  
Homo sapiens ring finger protein 28, mRNA (cDNA clone MGC:99548  
IMAGE:4862321), complete cds.  
BC080529  
BC080529.1 GI:51593348  
MGC.  
Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1764)

1 (bases 1 to 1764)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahy, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shchepochko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smailus, D.E.,  
Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

2 (bases 1 to 1764)  
Director MGC Project.  
Direct Submission  
Submitted (27-AUG-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@hgrl.nih.gov](mailto:nisc.mgc@hgrl.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lalic, P., Legaapi, R.,  
McDowell, J., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IBAL Plate: 59 Row: e Column: 1  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 19924162.

FEATURES

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Best Local Similarity 86.1%; Pred. No. 5.7e-176;		
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;		
QY	262	GACGAGGTGGGCAAGACAGTGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321
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DB	142	CCAGGATGGAAATCCCATGGAGAACTGGAGAGCAGCTGATCGCCCTATCTGCTGGA 201
QY	382	GATGTTTACCAAGCTGTGTCATCTGCTGCTGCCAACAACCTCTGCGGAGTGTGC 441
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DB	322	GTCGAGGCGCGTTTCGCTGCCCACTGCCGCCACGAGGTGATCATGGATCGTCACGG 381
QY	562	GGTGACGCGCTGCAGAGGAACTGCTGTTGGAAACATCATTGACATCTACAAGCAGGA 621
DB	382	AGTGACGCGCTGCAGAGGAACTGCTGTTGGAGAACATCATGCATCTACAAACAGGA 441
QY	622	GTCTCCAGTCGCGCCCTGCAGAAAGCAGCCACCGCATGTGCAAGAAACAGCAAGCA 681
DB	442	GTCTCCAGTCGCGCGCTGCAGAAAGGCGAGTCAACCCATGTGCAAGAGCAGCAAGATGA 501
QY	682	GAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTCTACTGCTCTTTGCAAGGTGT 741
DB	502	GAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTCTACTGCTCTTTGCAAGGTGT 561
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LOCUS		
DEFINITION Homo sapiens iris ring finger protein mRNA, complete cds.		
ACCESSION AF353673		
VERSION AF353673.1 GI:13785923		
KEYWORDS		
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ORGANISM		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 1791)		
AUTHORS Wistow,G.		
TITLE IRF: A Novel Ring Finger Protein From Iris		
JOURNAL Unpublished		
AUTHORS 2 (bases 1 to 1791)		
Wistow,G.		
TITLE Direct Submission		
JOURNAL Submitted (27-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD 20892, USA		
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ORIGIN

Query Match 50.2%; Score 802.2; DB 9; Length 1791;  
Best Local Similarity 86.1%; Pred. No. 5.7e-176;  
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 262 GACGAGGTGGGCAAGACAGTCCGCAATTTCAAAGCAATATGGATTTATAATCTAGCCTGAT 321  
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LOCUS Sequence 1222 from Patent EP1293569.  
DEFINITION AX714538  
ACCESSION AX714538  
VERSION AX714538.1 GI:29889491  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,  
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,  
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahara,K. and  
Masuho,Y.  
TITLE Full-length cDNAs  
JOURNAL Patent: EP 1293569-A 1222 19-MAR-2003;  
Helix Research Institute (JP) ; Research Association for  
Biotechnology (JP)  
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ORIGIN  
Query Match 50.1%; Score 800.6; DB 6; Length 1764;  
Best Local Similarity 86.0%; Pred. No. 1.4e-175;  
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DB |||||  
QY 220 GATGTTTACCAGCCAGTGGTCACTTCTGCTGCCAGCACAACTGTGCCGGAAGTGTC 279  
DB |||||  
QY 442 CAAACGACATCTTCCAGGCTGGCAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 501  
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QY 280 CAATGACATCTTCCAGGCTGCAAAATCCCTACTTGGACCAAGCGGCGAGCTCAGTGTCCAT 339  
DB |||||  
QY 502 GTCTGAGGCTGTTCCTGCTGCCCTCTGTCGCCCATGAAGTGATCATGGACCGGCAAG 561  
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QY 340 GTCTGAGGCGCTTTCCTGCTGCCCATCTGCCGCGCAGAGGTGATCATGGATCGTCACGG 399  
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QY 562 GGTTGACGCTGCAAGAGAACCTGCTGTGGTGAACATCATTTGACATCTACAAGCAGGA 621  
DB |||||  
QY 400 AGTTTACGGCTTGCAGAGGAACCTGCTGTGGTGAACATCATTCGACATCTACAAACAGGA 459  
DB |||||  
QY 622 GTGCTCCAGTGGGCCCCCTGCAGAAAGGAGCGCACCCGATGTGCAAGGAAACAGGAAGCA 681  
DB |||||  
QY 460 GTGCTCCAGTGGGCGCTGCAGAGGGCAGTCACCCCATGTGCAAGGAGCAGGAAGATGA 519  
DB |||||  
QY 682 GAAGATCAACATCTACTGCTCACTGTGAGTGCTTACTTGTCTCTCTCTCTCTCTCTCTCT 741  
DB |||||  
QY 520 GAAATCAACATCTACTGCTCACTGTGAGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 579  
DB |||||  
QY 742 TGGGCTCACCAGGCTGTGAGGTTGGCCCTTTGCAAGAGCATCTTCCAGAGGACAGGAAGAC 801  
DB |||||  
QY 580 TGGGATCACAAGGCTTGGAGGTGGCCCCCATTTGCAGAGTGTCTTCCAGGGACAAAGAC 639  
DB |||||

QY	802	TGAGCTGAGTAAGTCTCCATCTGCTGGTGGGGGAAACGACCGAGTGCAGACGATCAT	861
Db	640	TGAAGTGAATAAATGATCTCCATCTGCTGGTGGCGGGAATGACCGTGTGCAGACCATCAT	699
QY	862	CTTCTAGCTGGAGACTGCTGCAGAGTGCACCAAGGAGATAGCCACAGGTGAAGGAGGA	921
Db	700	CATCTAGCTGGAGGATTCCTCGTGCAGTGACCAAGGAGAACAGTTCACCGGTAAAGGA	759
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QY	982	GCAGCGGATCACGAGGAGGAGAGAGCTGGGCTTCATCGAGGCTCTTGATCTCTCCA	1041
Db	820	GCAGCGGATCACGAGGAGGAGAGAAAGCTTAGCTTCATCGAGGCTCTCATCCAGCA	879
QY	1042	GTCAGGAGGAGCTGGAAGTCCACCAAGCTTGTGGAGACCGCATTCAGTCCCTGGA	1101
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QY	1102	TGAGCCCGAGGGGCTTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATCTGAGA	1161
Db	940	CGAGCTTGGGAGGCCACCTTCTCTTCTGACTGCAAGCAACTCATCAAGCAATTTGGA	999
QY	1162	AGCTTCCAAGGGTGCAGCTGGGGAAGACAGCAAGGCTTTGAGAACATGGACTACTT	1221
Db	1000	AGCTTCCAAGGGTGCAGCTGGGGAAGACAGAGCAGGCTTTGAGAACATGGACTTCT	1059
QY	1222	TACTCTGACTTAGACACATAGCAGAGGCTTGAGGGCCATTTGAGGACAGGTAA	1281
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QY	1282	AGGATGTGATG 1292	
Db	1120	GGAGAGGAAG 1130	

RESULT 10	AK056942	Homo sapiens cDNA FLJ32380 fis, clone SKMUS1000064, moderately similar to Mus musculus RING-finger protein MURF mRNA.	PRI 30-JAN-2004
LOCUS	AK056942		
DEFINITION	AK056942		
ACCESSION	AK056942.1	GI:16552479	
VERSION			
KEYWORDS		oligo capping; fis (full insert sequence).	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oyamashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, K., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Kumagai, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Sugai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, K., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,	

Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isegai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs	Nat. Genet. 36 (1), 40-45 (2004)		
JOURNAL	14702039		
PUBMED			
REFERENCE			
AUTHORS			
Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isegai, T.			
NEDO human cDNA sequencing project			
Unpublished			
3 (bases 1 to 1764)			
Isogai, T., Otsuki, T. and Sugiyama, T.			
Direct Submission			
Submitted (24-OCT-2001) Takao Isegai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.			
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Query Match 50.1%; Score 800.6; DB 9; Length 1764; Best Local Similarity 86.0%; Pred. No. 1.4e-175; Matches 887; Conservative 0; Mismatches 144; Indels 0; Gaps 0;			
QY 262 GACGAGGTGGGCAAGACAGATCGCATTTTCAAAGCAATATGGATTATAAATCTAGCCTGAT	321		
Db 100 GAGGACGTAGCGGTGGCTCTCATCTTCCCAACAGATGGATTATAAGTCGAGCCTGAT	159		
QY 322 TCCTGATGAAACGCTATGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTGCTCGGA	381		
Db 160 CCAGGATGGAATCCATGGAGAACTTGAGAGAGCAGCTGATCTGCCCTATCTGCCCTGA	219		
QY 382 GATGTTTACCAAGCCTGGTGGTTCATCTGCCCTGCCACCAACCTCTGCCGGAAGTGTGC	441		
Db 220 GATGTTTACCAAGCAGGTGGTTCATCTTCCGCGTCCGACGACCAACCTGTGCCGGAAGTGTGC	279		

REFERENCE	1 (bases 1 to 1041)
AUTHORS	Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
TITLE	Cloning of human full-length CDSs in BD Creator(TM) System Donor vector
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1041)
AUTHORS	Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT	This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
FEATURES	Location/Qualifiers
source	1..1041
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	/lab_host="DHSalpha T1 resistant"
	/note="Vector: pDNR-Dual"
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ORIGIN	
Query Match	50.0%; Score 799.2; DB 9; Length 1041;
Best Local Similarity	87.7%; Pred. No. 2.8e-175;
Matches	873; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
Qy	299 ATGATTAATAATCTAGCCTGATTCCTCATGGAACGCTATGAGAACCTGAGAGACGAG 358
Db	1 ATGATTAATAAGTCAGCCTGATCCAGGATGGGAATCCCATGAGAACCTTGGAGAACGAG 60
Qy	359 CTGATCTCCCCCATCTGCTGGAGATGTTTACCAAGCCTGTGTGTCATCTGCGCTGCCAA 418
Db	61 CTGATCTCCCATCTGCTGGAGATGTTTACCAAGCAGTGTGTCTCTTGGCGTGCAG 120
Qy	419 CACAACTCTGCGGAGAGTGTGCAACGACATCTTCCAGGCTGCGAAATCCCTACTGGACC 478
Db	121 CACAACTGTGCGGAGAGTGTGCCAATGACATCTTCCAGGCTGCAAAATCCCTACTGGACC 180
Qy	479 AACCGCGTGTGCTCAGTGTCCATGTCTGAGGTGCTTTCCGTTGCCCTCGTCCGCCCAT 538
Db	181 AGCCGGGCGAGCTCAGTGTCCATGTCTGAGGCGCGTTCGCTGCCCACTTGCCTGCCAC 240
Qy	539 GAAGTGATCATGGACCGGCGACCGGGGTGTACGGCTTCGACAGGAACCTGTGTGGAAAC 598
Db	241 GAGGTGATCATGGATCGTCACGGAGTGTACGGCTCTGACAGGAACCTGTGTGGAGAAC 300
Qy	599 ATCATTGATCATTCACAGCAGGAGTGTCTCCAGTCCGCGCCCTTCGAGAGAACGACGCCACC 658

Db	301	ATCATGCACATCTACAAACAGGAGTGTCTCCAGTCCGCGCTGCAGAAAGGCGAGTCACCC	360
Qy	659	ATGTGCAAGGAACACGACGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCCT	718
Db	361	ATGTGCAAGGAGACCAAGATGAGAAATCAACATCTACTGTCTCAGTGTGAGGTGCC	420
Qy	719	ACTTGTCTCTTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCCCCCTTGGCAA	778
Db	421	ACCTGTCTCATGTGCAAGGTGTTGGATCCCAAGGCTGCAGGTGCCCCCATTTGCAG	480
Qy	779	AGCATCTTCCAAGCAGACAGACTGAGCTGAGTGAAGTCACTCTCCATCTGCTGTGGCGGG	838
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Qy	839	ACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGACTCTGTCAGAGTACCAAGGAG	898
Db	541	AATGACCGTGTGCAGACCATCATCACTCACTGAGGTGATTCGCTCGAGTACCAAGGAG	600
Qy	899	AATAGCCACAGGTGAAGGAGGCTGAGTCAAGTGTGACACCTCTACGCCATCTCTG	958
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Qy	959	GATGAGAAGAGCAGCTGTCTGCAGCGGATCACGACGAGCAGAGGAGCTGGGC	1018
Db	661	GATGAGAAGAAAGTGAAGTGTCTGCAGCGGATCACGACGAGCAGAGGAGAAAGCTTAG	720
Qy	1019	TTTCATCGAGCTCTGATCTCTCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG	1078
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Qy	1079	GAGACCGCATTCAGTCCCTTGATGAGCCGAGGAGGCTACCTTCTCTCAAGTGCACAAG	1138
Db	781	GAACTGCCATCAGTCCCTTGACGAGCTTGGGAGACCACTTCTCTTGACTGCCAAG	840
Qy	1139	CAGCTCATCAAGACATTTGAGAGCTTCAAGGCTTCAAGGCTGCAGTGGGGAAGACAGCAA	1198
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Qy	1199	GGCTTTGAGACATGACTACTTCTGACTAGACATAGACAGGAGCTTGGAG	1258
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Qy	1259	GCCATTGACTTTGGGACAGGTAAGCATGTGATGTT	1294
Db	961	GCCATTGACTTTGGGCGAGCTGAAGTATGAGAT	996
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LOCUS			
DEFINITION	BT008198 1041 bp mRNA linear SYN 13-MAY-2003		
ACCESSION	Synthetic construct Homo sapiens ring finger protein 28 mRNA,		
VERSION	partial cds.		
KEYWORDS	BT008198.1 GI:30585234		
SOURCE	FLI CDNA.		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1 (bases 1 to 1041)		
TITLE	Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,		
JOURNAL	Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,		
REFERENCE	Phelan,M. and Farmer,A.		
AUTHORS	Cloning of human full-length CDSs in BD Creator (TM) System Donor		
TITLE	vector		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1041)		
AUTHORS	Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,		
TITLE	Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,		
JOURNAL	Phelan,M. and Farmer,A.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow		
TITLE	Circle, Palo Alto, CA 94303, USA		

COMMENT	This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.		
FEATURES	Location/Qualifiers		
source	1..1041		
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	SVFQKQSTLNLCISMLVAGNDVQTIITQLEDSRRVTKENSHPVKEELSKQFDTLYA		
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ORIGIN			
Query Match	50.0%;	Score 799.2;	DB 12; Length 1041;
Best Local Similarity	87.7%;	Pred. No. 2.8e-175;	
Matches	873;	Conservative	0; Mismatches 123; Indels 0; Gaps 0;
Qy	299	ATGGATTATAATCTAGCCTGATTCCTGATGAAGACGCTATGGAGAACCTGGAGAACGAG	358
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Qy	419	CACAACTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478
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Qy	479	AACCGGCTGGCTCAGTGTCCATGTCTGGAGTGTTCCTGCTGCCCTCGTGGCCCAT	538
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Qy	539	GAAGTGATCATGACCGCGCGGTGTACGCGCTGCAGAGGAACCTGCTGGTGGAAAC	598
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Qy	719	ACTTGTCTCTTGTGCAAGGTGTTGGGCTCACCAAGGCTGTGAGGTTCGCCCTTTGCCAA	778
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Qy 959 GATGAGAGAGAGCGAGCTGCTGACGCGGATCAGCAGGAGCAGGAGGAGAGCTGGCG 1018
Db 661 GATGAGAGAAAGTGAAGTGTCTGACGCGGATCAGCAGGAGCAGGAGGAGAAAGCTTAGC 720
Qy 1019 TTCACTCGAGGCTCTCATCTCTCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTTGTG 1078
Db 721 TTCACTCGAGGCTCTCATCCAGCAGTACAGGAGCAGCTGGACAGTCCACCAAGCTGGTG 780
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Db 841 CAACTCATCAAGCATTTGTGAAGCTTCCAAAGGCTGCGCAGCTGGGGAAGACAGAGCAG 900
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RESULT 13
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LOCUS AR220796 1757 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 37 from patent US 6426186.
ACCESSION AR220796
VERSION AR220796.1 GI:23327673
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1757)
AUTHORS Jones, K.A., Volkmut, W. and Walker, M.G.
TITLE Bone remodeling genes
JOURNAL Patent: US 6426186-A 37 30-JUL-2002;
FEATURES
source 1..1757
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ORIGIN
Query Match 46.8%; Score 747.8; DB 6; Length 1757;
Best Local Similarity 82.8%; Pred No. 2.7e-163;
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 262 GAGCAGGTGGGCAAGACAGTCCGATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321
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Qy 322 TCCTGATGAAAGCTGTGGAGAACCTGGAGAGCAGTGAATCTGCCCATCTGCTGGA 381
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VERSION AX576231.1 GI:27645982
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Banville, S.C., Greenawalt, L.B., Lincoln, S.E., Stockdrehner, T.K.,
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Amshey, S., Chang, S.C., Chen, W., Dam, T.C., Liu, T.F., Rosen, B.H., Russo, F.D., D'Sa, S.A., Spiro, P.A., Bradley, D.L., Chen, A., Cohen, H.J., Daffo, A., Daniels, S.E., Dufour, G.E., Flores, V., Fong, W.T., Hodgson, D.M., Jackson, S., Jones, A.L., Panzer, S.R., Roseberry, A.M., Shah, P., Wright, R.J., Yap, P.E., Yu, J.Y., Bratcher, S.R., Chalup, M.S., Dahl, C.R. and Hallman, J.L.  
**TITLE**  
 Polypeptides and corresponding molecules for disease detection and treatment  
**JOURNAL**  
 Patent: WO 0162922-A 12 30-AUG-2001;  
 Incyte Genomics, Inc. (US)  
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 Best Local Similarity 82.8%; Pred. No. 2.7e-163;  
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 ACCESSION BX929474  
 VERSION BX929474.1 GI:41629941  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 1 (bases 1 to 1248)  
 Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E.,  
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 Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R.,  
 Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G.,  
 Tickle, C. and Wilson, S.A.  
 Direct Submission  
 Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: chickens@ms.unist.ac.uk  
 BBSRC/Dunelm/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA  
 sequencing project.  
 This sequence is from the  
 BBSRC/Dunelm/Nottingham/Sanger/Sheffield/UMIST cDNA collection,  
 from a library constructed by Elizabeth Bosch. cDNA was prepared  
 from RNA extracted from muscle, normalised, and poly A-trimmed.  
 EcoRI-NotI cut cDNA was then ligated into the vector. Vector:  
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**ORIGIN**  
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 Best Local Similarity 76.7%; Pred. No. 4.6e-132;  
 Matches 764; Conservative 0; Mismatches 229; Indels 3; Gaps 1;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:39:05 ; Search time 299 Seconds  
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Title: US-10-775-649-5

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Searched: 1202784 seqs, 818138359 residues

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Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Sequence 5, Application US/09908988B

; Patent No. 6740751

; GENERAL INFORMATION:

; APPLICANT: OLSON, ERIC

; APPLICANT: SPENCER, JEFFREY A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES

; FILE REFERENCE: MYOG:028US

; CURRENT APPLICATION NUMBER: US/09/908,988B

; CURRENT FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: 60/219,020

; PRIOR FILING DATE: 2000-07-18

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 1597

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (299)..(1327)

US-09-908-988B-5

Query Match

Best Local Similarity 100.0%; Score 1597; DB 4; Length 1597;

Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmoth, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
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; LENGTH: 1757  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 247384.1CB1  
US-09-484-970B-37

Query Match 46.8%; Score 747.8; DB 3; Length 1757;  
Best Local Similarity 82.8%; Pred. No. 6.4e-205;  
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 262 GACGAGGTGGGCAAGACAGATCGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321  
Db 88 GAGGAGCTAGGGTGGCTCTCATCTTCCACAGAAATGGATTATAAGTCGAGCCTGAT 147  
Qy 322 TCTGATGAAAACGCTATGAGAACTTGAGAAAGAGCTGATCTGCCCCATCTGCCCTGGA 381  
Db 148 CCAGGATGGGAATCCCATGGAGAACTTGAGAAAGCAGCTGATCTGCCCTATCTGCCCTGGA 207  
Qy 382 GATGTTTACCAAGCCTGTGCTCATCTGCCCTGCCAACACCACTCTGCCGGAAGTGC 441  
Db 208 GATGTTTACCAAGCAGTGGTCACTTGCCTGCGCAGCAACCTCTGCCGGAAGTGC 267  
Qy 442 CAACGACATCTTCCAGGCTGCGAATCCCTACTGCGACCAACCCGCGTGGCTCAGTGTCCAT 501  
Db 268 CAATGATATTTCCAGGCTCTTAAACCGTATTTGGCCCAAGAGGAGGTACCAACCATGGC 327  
Qy 502 GTCTGAGGTGCTGTTCCGTTGCCCTCTGTCGCCCATGAAAGTGTATCATGGAACCGGACGG 561  
Db 328 ATCAGGGGCGCATCTCCGCTGCCCATCTCTGTAGACATGAAAGTGGTTTTGTAGACATGG 387  
Qy 562 GGTGTACGCGCTGCAGAGGAACCTGCTGTTGAAACATCATTTGACATCTACAAGCAGGA 621  
Db 388 GGTATATGACTTTCAGAGGAACCTGCTGTTGGAACATCATCGACATCTACAACAGGA 447  
Qy 622 GTGCTCCAGTCGGCCCCCTGCAGAAAAGGAGCCACCGCATGTGCAAGGAACACGAAGACGA 681  
Db 448 GTGCTCCAGTCGGCGCTGCAGAAAGGAGTCAACCCCATGTGCAAGGAGACGAAGATGA 507  
Qy 682 GAAATCAACATCTACTGTCTCAAGTGTGAGGTGCTTCTCTCTGTCGAAAGTGT 741  
Db 508 GAAAATCAACATCTACTGTCTCAAGTGTGAGGTGCTTCTCTCTGTCGAAAGTGT 567



APPLICANT: SPENCER, JEFFREY A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
FILE REFERENCE: MYOG:028US  
CURRENT APPLICATION NUMBER: US/09/908,988B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: 60/219,020  
PRIOR FILING DATE: 2000-07-18  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2590  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (80)..(1714)  
US-09-908-988B-3

Query Match 27.1%; Score 432.2; DB 4; Length 2590;  
Best Local Similarity 66.5%; Pred. No. 7.5e-114;  
Matches 636; Conservative 0; Mismatches 318; Indels 3; Gaps 1;

QY 336 CTATGGAGAACTGGAGAACGACGTGATCTGCCCATCTCCCTGGAGATGTTTACCAAGC 395  
DB 126 CCATGGATAACTTGGAAAGCAACTGATCTGTCCATCTGCTTAGAGATGTTTACGAAGC 185  
QY 396 CTGTGGTCATCTCCCTCCCAACACACACACCTCTGCCGGAAGTGTGCCAAGACATCTTC 455  
DB 186 CTGTGGTCATCTCCCTTGGCCAGCACAACTGTGCAGGAATGTGCCAGTGACATCTTC 245  
QY 456 AGGTGCGAATCCCTACTCTGACCAACCGCGTGGCTCAGTGTCCATGTCTGGAGGTGCTT 515  
DB 246 AGGCTCTAACCGTACTTACCCACAGAGAGAGCCACCCTGGCATCAGGGGGCGCT 305  
QY 516 TCCGTTGCCCTCGTCCGCCATGAAGTGAATCATGACACATCTACAGCAGGAGTGTCCAGTCCGC 635  
DB 366 AGAGGAACCTGCTCGTGGAAAAATTATGATATCTACAGCAGGAATCCACCA---GGC 422  
QY 636 CCCTGCAAGAAAGGAGCAGCCACCCATGTGCAAGGAACACGAGAGACGAGAAATCAACATCT 695  
DB 423 CAGAAAAAATTGGACCAACCCATGTGTGAAGGATGAAGAGAACGATCAACATCT 482  
QY 696 ACTGTCTCAGTGTGAGTGCCTTCTGCTTGTGCAAGGTGTTTGGGGCTCAACGAG 755  
DB 483 ATTGTCTGAACTGTGAAGTGCACCACTGTCTTGTGCAAGGTTTTTGGCGCCATAAGG 542  
QY 756 CTTGTGAGGTGTCCTTTGCAAGCATCTTCCAGCAGAGAGACTGAGCTGAGTAAC 815  
DB 543 ACTGCCAGGTGGTCTCCCTGACTCATGTGTGTCCAGAGGCAAGATCAGAGCTCAGTGATG 602  
QY 816 GCATCTCCATGCTGTGGCGGGGAAACGACGAGTGCAGACGATCATCTCTCAGCTGGAGG 875  
DB 603 GTATTGTGTACTTGTGGGAAGCAACGATAGATCCAGGGTGTGATCAGCCAGCTGGAGG 662  
QY 876 ACTGTGTCAGAGTGACCAAGGAGAAATAGCCACGAGTGAAGAGGAGCTGAGTCAGAA 935  
DB 663 ACACCTGTAAACATTATTGAGGAGTGTCTGCAAGAAAGCAGAAACAGGACCTGTGTGAGAA 722  
QY 936 TTCACACCTCTAGCCATCCTGGATGAGAGAGAGCGAGCTGTCAGCGGATCAGCG 995  
DB 723 TTGATCACCTATACGGCATCTGGAGGAGGAAGACTGAAATGACCCAGGCCATCCTC 782  
QY 996 AGGAGCAGGAGGAGAGCTGGGCTTATCAGAGCTCTGATCTCCAGTACAGGAGCAGC 1055  
DB 783 GACACAGAGGAGAGAACTGGAACATGTCGCACTCTTATCAGGAAGTATTCGATCACC 842  
QY 1056 TGGAAAGTCCCAAGCTGTGTGGAGACCCGCAATCCAGTCCCTGGATGAGCCCGGAGGGG 1115

DB 843 TGGAGAACTGATCCAAAGTTGGTGGAGTCAGGAATCCAGTTCTGGATGAGCCGCAATGG 902  
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DB 903 CAGTATTTCTGCAGAAATGCCAAGCCCTGTTGCAAAAGATCGTGGAGCATCAAGGCGT 962  
QY 1176 GCCAGCTGGGAAGACAGACGAGCAAGGCTTTGAGAACATGAGCTACTTTACTCTGGACTTAG 1235  
DB 963 TTCAGATGGAGAACTAGAACAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCA 1022  
QY 1236 AACACATAGCAGAGCGCTTTGAGGGCCATTTGACTTTTGGGACAGGTAAGGATGTGATG 1292  
DB 1023 ATAGAGAGAAAAAATTATCCGTGAAATTTGACTTTTCTAGAGAGAGGAGAGGAAG 1079

RESULT 5  
US-09-949-016-13746/c  
Sequence 13746, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13746  
LENGTH: 4867  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-13746

Query Match 6.9%; Score 109.8; DB 4; Length 4867;  
Best Local Similarity 67.0%; Pred. No. 9.3e-21;  
Matches 156; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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QY 954 TCTGTGATGAGAAAGAGAGCGAGCTGCTGACGGATCACGAGGAGCAGGAGGAGAGC 1013  
DB 4621 TGTGGAGGAGCGCAAGGCTGAGCTGCTGACGGCTGGCCCGGAGCAAGAGGAGAGC 4562  
QY 1014 TGGCTTTCATCAGAGCTGTGATCTCTCCAGTACAGGAGCAGCTGGAAGAAAGTCCACCAAGC 1073  
DB 4561 TGCAGCGCTGCGCGGCTCATCCGTCAGTATGGCGACCACTCTGGAGGCTCTCTTAAGC 4502  
QY 1074 TTGTGAGACCGCATCCAGTCCCTGATGAGCCGAGGGGCTACCTTCTCCTC 1126  
DB 4501 TGTGTGAGTCTGCCATCCAGTCCATGGAAGAGCCACAAATGGCGCTGTATCTC 4449

RESULT 6  
US-09-561-989-9  
Sequence 9, Application US/09561989  
Patent No. 6468750  
GENERAL INFORMATION:  
APPLICANT: KOLLER, Klaus-Peter  
TITLE OF INVENTION: No. 6468750e1 Cell Regulation Factor T7020  
FILE REFERENCE: seq  
CURRENT APPLICATION NUMBER: US/09/561,989  
CURRENT FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 11:08:50 ; Search time 918 Seconds  
(without alignments)  
10784.204 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597  
Sequence: 1 ctcgagattacccttacg.....gaaataaattctcgtgcc 1597

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6046767 seqs, 309930249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1597	100.0	1597	9	US-09-908-988B-5 Sequence 5, Appli
2	1597	100.0	1597	19	US-10-775-649-5 Sequence 5, Appli
3	1597	100.0	1597	15	US-10-775-627-5 Sequence 20, Appli
4	890.8	55.8	1053	15	US-10-061-043A-20 Sequence 20, Appli
5	890.8	55.8	1053	17	US-10-060-634C-20 Sequence 20, Appli
6	803.8	50.3	2097	15	US-10-061-043A-22 Sequence 22, Appli
7	803.8	50.3	2097	17	US-10-060-634C-22 Sequence 22, Appli

8	802.2	50.2	1764	18	US-10-221-625-192 Sequence 182, App
9	802.2	50.2	2700	20	US-10-723-860-7801 Sequence 7801, Ap
10	800.6	50.1	1764	17	US-10-094-749-1222 Sequence 1222, Ap
11	797.4	49.9	1781	9	US-09-764-864-21 Sequence 21, Appl
12	747.8	46.8	2110	21	US-10-204-921-12 Sequence 12, Appl
13	547.4	34.3	630	15	US-10-061-043A-32 Sequence 32, Appl
14	547.4	34.3	630	17	US-10-060-634C-32 Sequence 32, Appl
15	484.6	30.3	1431	9	US-09-908-988B-1 Sequence 1, Appli
16	484.6	30.3	1431	19	US-10-775-649-1 Sequence 1, Appli
17	484.6	30.3	1431	19	US-10-775-627-1 Sequence 57, Appl
18	481.8	30.2	1913	10	US-09-890-688-57 Sequence 38, Appl
19	444.4	27.8	867	15	US-10-061-043A-38 Sequence 38, Appl
20	444.4	27.8	867	17	US-10-060-634C-38 Sequence 3, Appli
21	432.2	27.1	2590	9	US-09-908-988B-3 Sequence 3, Appli
22	432.2	27.1	2590	19	US-10-775-649-3 Sequence 3, Appli
23	432.2	27.1	2590	19	US-10-775-627-3 Sequence 673, App
24	430.6	27.0	1925	17	US-10-104-047-673 Sequence 36, Appl
25	430.6	27.0	2434	19	US-10-473-574-36 Sequence 433, App
26	430.6	27.0	2634	17	US-10-104-047-433 Sequence 7135, Ap
27	430.6	27.0	2662	20	US-10-723-860-7135 Sequence 34, Appli
28	421.2	26.4	1762	9	US-09-764-864-34 Sequence 6101, Ap
29	390	24.4	531	11	US-09-864-408A-6101 Sequence 22, Appl
30	329.4	20.6	2040	18	US-10-250-613-22 Sequence 25, Appl
31	277	17.3	1039	9	US-09-880-192-25 Sequence 25, Appl
32	277	17.3	1039	16	US-10-427-348-25 Sequence 5316, Ap
33	260.6	16.3	424	10	US-09-918-595-5316 Sequence 4809, Ap
34	246.4	15.4	411	10	US-09-918-595-4809 Sequence 482, App
35	244.2	15.3	446	9	US-09-764-864-482 Sequence 493, App
36	217.8	13.6	587	9	US-09-764-864-493 Sequence 895, App
c 37	156.8	9.8	638	17	US-10-191-803-895 Sequence 7957, Ap
38	141.6	8.9	766	20	US-10-723-860-7957 Sequence 10290, A
c 39	141.6	8.9	2000	14	US-10-198-846-10290 Sequence 4075, Ap
40	123.4	7.7	475	20	US-10-723-860-4075 Sequence 1109, Ap
41	101.4	6.3	3127	17	US-10-108-260A-1109 Sequence 32020, A
42	100.2	6.3	498	10	US-09-918-995-32020 Sequence 83161, A
43	87.4	5.5	728	20	US-10-425-115-83161 Sequence 9, Appli
44	86.6	5.4	3262	14	US-10-237-790-9 Sequence 407, App
45	86.6	5.4	3480	18	US-10-302-172-407

ALIGNMENTS

RESULT 1

US-09-908-988B-5  
; Sequence 5, Application US/09908988B  
; Patent No. US20020127690A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSON, ERIC  
; APPLICANT: SPENCER, JEFFREY A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
; FILE REFERENCE: MYOG:028US  
; CURRENT APPLICATION NUMBER: US/09/908,988B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/219,020  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1597  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (299)..(1327)  
US-09-908-988B-5

Query Match 100.0%; Score 1597; DB 9; Length 1597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GGNACGGGACGCGAAGGAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCTCAAGAGCA 120  
Qy 121 GCAGACATGAGTAATCTTGGAAGCAACTGATCTGTCCCATCTGCTAGAGATGTTTAC 180  
Db 121 GCAGACATGAGTAATCTTGGAAGCAACTGATCTGTCCCATCTGCTAGAGATGTTTAC 180  
Qy 181 GAAGCCTGTGTCAATCTCCCTTGGCCAGCAACAACCTGTGAGGAATGTGCGGCCCCCCC 240  
Db 181 GAAGCCTGTGTCAATCTCCCTTGGCCAGCAACAACCTGTGAGGAATGTGCGGCCCCCCC 240  
Qy 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTCGCATTTCAAGCAATAT 300  
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Qy 301 GGATTATAATCTAGCTCTGATTCCTGATGGAAACGCTATGGAAACCTGGAGAGCAGCT 360  
Db 301 GGATTATAATCTAGCTCTGATTCCTGATGGAAACGCTATGGAAACCTGGAGAGCAGCT 360  
Qy 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTCATCTGCCCTGCCAACA 420  
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Qy 421 CAACCTCTGCCGGAAGTGTGCAACACATCTTCCAGGCTGGAATCCCTACTGGACCAA 480  
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Qy 481 CCGCGTGGCTCAGTCTCATGCTCGAGGTGCTTTCCGTTGCGCTCGTGGCCCATGA 540  
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Qy 541 AGTGATCTGAGACCGGCAAGGCTGTACCGGCTGACAGAGAACTCTCTGTTGGAACAAT 600  
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Qy 601 CATTGACATCTAAGCAGAGTGTCCAGTGGGCTGCGGCTGCAAGAGGAGCCAGCT 660  
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Qy 661 GTCAAGGAAACAGAAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTAC 720  
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Qy 721 TTGCTCCTTGTCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCTTGTGCAAG 780  
Db 721 TTGCTCCTTGTCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCTTGTGCAAG 780  
Qy 781 CATCTTCCAAAGGACAGAGCTGAGTGAATCTGCATCTCCATCTGCTGGTGGCGGAA 840  
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Qy 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGACCAAGAGAA 900  
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Qy 961 TGAGAGAGAGAGAGCTGCTGAGCGGATCAGCAGGAGCAGGAGAGAGTGGCTT 1020  
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Qy 1081 GACCGCATCTCAGTCTGATGAGCCCGGAGGGGCTACTCTTCTCTCAAGTGCACAGCA 1140

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Qy 1261 CATTGACCTTTGGGACAGGTAAAGATGTGATGTTTACATGTTTGAACCTTTGAAAGCAGCG 1320  
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Qy 1381 AGGTCTCTCTATGAGGCTGACTGCTTGTAGTAGTGTCTTAAAGTAAAGTAAATTTACACAGCAGTGTGAC 1440  
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Db 1561 TGGTACATAATTTGTTTTCGAAATAAATTTATCTCTGCTGCC 1597

RESULT 2  
US-10-775-649-5  
; Sequence 5, Application US/10775649  
; Publication No. US20040132160A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSON, ERIC  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROFIBULES  
; FILE REFERENCE: MYOG:028USD2  
; CURRENT APPLICATION NUMBER: US/10/775,649  
; CURRENT FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 09/908,988  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: 60/219,020  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1597  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (299) .. (1327)  
US-10-775-649-5

Query Match 100.0%; Score 1597; DB 19; Length 1597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GGNACGGGACGCGAAGGAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCTCAAGAGCA 120  
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Db 181 GAAGCCTGTGTCAATCTCCCTTGGCCAGCAACAACCTGTGAGGAATGTGCGGCCCCCCC 240  
Qy 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTCGCATTTCAAGCAATAT 300  
Db 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTCGCATTTCAAGCAATAT 300  
Qy 301 GGATTATAATCTAGCTCTGATTCCTGATGGAAACGCTATGGAAACCTGGAGAGCAGCT 360  
Db 301 GGATTATAATCTAGCTCTGATTCCTGATGGAAACGCTATGGAAACCTGGAGAGCAGCT 360  
Qy 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTCATCTGCCCTGCCAACA 420  
Db 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTCATCTGCCCTGCCAACA 420  
Qy 421 CAACCTCTGCCGGAAGTGTGCAACACATCTTCCAGGCTGGAATCCCTACTGGACCAA 480  
Db 421 CAACCTCTGCCGGAAGTGTGCAACACATCTTCCAGGCTGGAATCCCTACTGGACCAA 480  
Qy 481 CCGCGTGGCTCAGTCTCATGCTCGAGGTGCTTTCCGTTGCGCTCGTGGCCCATGA 540  
Db 481 CCGCGTGGCTCAGTCTCATGCTCGAGGTGCTTTCCGTTGCGCTCGTGGCCCATGA 540  
Qy 541 AGTGATCTGAGACCGGCAAGGCTGTACCGGCTGACAGAGAACTCTCTGTTGGAACAAT 600  
Db 541 AGTGATCTGAGACCGGCAAGGCTGTACCGGCTGACAGAGAACTCTCTGTTGGAACAAT 600  
Qy 601 CATTGACATCTAAGCAGAGTGTCCAGTGGGCTGCGGCTGCAAGAGGAGCCAGCT 660  
Db 601 CATTGACATCTAAGCAGAGTGTCCAGTGGGCTGCGGCTGCAAGAGGAGCCAGCT 660  
Qy 661 GTCAAGGAAACAGAAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTAC 720  
Db 661 GTCAAGGAAACAGAAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTAC 720  
Qy 721 TTGCTCCTTGTCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCTTGTGCAAG 780  
Db 721 TTGCTCCTTGTCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCTTGTGCAAG 780  
Qy 781 CATCTTCCAAAGGACAGAGCTGAGTGAATCTGCATCTCCATCTGCTGGTGGCGGAA 840  
Db 781 CATCTTCCAAAGGACAGAGCTGAGTGAATCTGCATCTCCATCTGCTGGTGGCGGAA 840  
Qy 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGACCAAGAGAA 900  
Db 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGACCAAGAGAA 900  
Qy 901 TAGCCACCAAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGAACCCCTCTACGCCCATCTCGA 960  
Db 901 TAGCCACCAAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGAACCCCTCTACGCCCATCTCGA 960  
Qy 961 TGAGAGAGAGAGAGCTGCTGAGCGGATCAGCAGGAGCAGGAGAGAGTGGCTT 1020  
Db 961 TGAGAGAGAGAGAGCTGCTGAGCGGATCAGCAGGAGCAGGAGAGAGTGGCTT 1020  
Qy 1021 CATCGAGGCTCTGATCTCTCAGTACAGGAGAGCTGGAAGTCCCAAGTCTGTGA 1080  
Db 1021 CATCGAGGCTCTGATCTCTCAGTACAGGAGAGCTGGAAGTCCCAAGTCTGTGA 1080  
Qy 1081 GACCGCATCTCAGTCTGATGAGCCCGGAGGGGCTACTCTTCTCTCAAGTGCACAGCA 1140

QY 121 GCAGACCATGATTAACCTTGGAAAAAGCAACTGATCTGTCTCCATCTGCCTTAGAGATGTTCCAC 180  
DB 121 GCAGACCATGATTAACCTTGGAAAAAGCAACTGATCTGTCTCCATCTGCCTTAGAGATGTTCCAC 180  
QY 181 GAAGCCTGTGCTATCTCCCTTGCAGACCAACCTGTGCAGGAATGTGGGGCCCCC 240  
DB 181 GAAGCCTGTGCTATCTCCCTTGCAGACCAACCTGTGCAGGAATGTGGGGCCCCC 240  
QY 241 TTGGAGACAAAGACTTGTGTGACCGCAGGTGGCAAGACAGTCGATTTCAAAGCAATAT 300  
DB 241 TTGGAGACAAAGACTTGTGTGACCGCAGGTGGCAAGACAGTCGATTTCAAAGCAATAT 300  
QY 301 GGATTTAAATCTAGCCTGATTTCTGTATGGAAAAAGCTATGAGAAACCTGGGAAGCAGCT 360  
DB 301 GGATTTAAATCTAGCCTGATTTCTGTATGGAAAAAGCTATGAGAAACCTGGGAAGCAGCT 360  
QY 361 GATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCTGTGCTATCTGCCTGCCCAACA 420  
DB 361 GATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCTGTGCTATCTGCCTGCCCAACA 420  
QY 421 CAACCTCTGCCGGAAGTGTGCAACAGCATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480  
DB 421 CAACCTCTGCCGGAAGTGTGCAACAGCATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480  
QY 481 CCGGGTGGCTCAGTGTCCATGTCTGGAGGTGTTTTCCGTTGCCCCCTGCGCCATGA 540  
DB 481 CCGGGTGGCTCAGTGTCCATGTCTGGAGGTGTTTTCCGTTGCCCCCTGCGCCATGA 540  
QY 541 AGTGATCATGACCGGACCGGGGTGTACGGCTGCAGAGGAACCTGCTGGTGGAAAAAT 600  
DB 541 AGTGATCATGACCGGACCGGGGTGTACGGCTGCAGAGGAACCTGCTGGTGGAAAAAT 600  
QY 601 CATTGACATCTACAGCAGGAGTGTCTCAGTCCGGCCCTGCAGAAAGCAGCACCCGAT 660  
DB 601 CATTGACATCTACAGCAGGAGTGTCTCAGTCCGGCCCTGCAGAAAGCAGCACCCGAT 660  
QY 661 GTGCAAGGAACACGAAAGCAGGAAGATCAACATCTACTCTACTCTCAGCTGTGAGGTGCTTAC 720  
DB 661 GTGCAAGGAACACGAAAGCAGGAAGATCAACATCTACTCTACTCTCAGCTGTGAGGTGCTTAC 720  
QY 721 TTGCTCTTGTGCAAGTGTGTTGGGGCTCACAGGCCCTGTGAGGTGCCCCCTTGTGCAAG 780  
DB 721 TTGCTCTTGTGCAAGTGTGTTGGGGCTCACAGGCCCTGTGAGGTGCCCCCTTGTGCAAG 780  
QY 781 CATCTTCCAAGACAGAAAGACTGAGTGAATGCACTCCATGCTGCTGGGGGAA 840  
DB 781 CATCTTCCAAGACAGAAAGACTGAGTGAATGCACTCCATGCTGCTGGGGGAA 840  
QY 841 CGACGAGTGCAGACGATCATCTCTCAGCTGGAGACTCGTGACAGAGTGACCAAGGAA 900  
DB 841 CGACGAGTGCAGACGATCATCTCTCAGCTGGAGACTCGTGACAGAGTGACCAAGGAA 900  
QY 901 TAGCCACAGGTGAGGAGGAGTCACTGATCAGAGTTTGACACCCCTCTACGCCATCTCTGA 960  
DB 901 TAGCCACAGGTGAGGAGGAGTCACTGATCAGAGTTTGACACCCCTCTACGCCATCTCTGA 960  
QY 961 TGAGAAAGAGCAGAGTGTGTCAGCGGATCACGAGCAGAGGAGGAGAGCTGGGCTT 1020  
DB 961 TGAGAAAGAGCAGAGTGTGTCAGCGGATCACGAGCAGAGGAGGAGAGAGCTGGGCTT 1020  
QY 1021 CATCGAGCTCTGATCTCTCCAGTACAGGAGCAGCTGGAAAAAGTCCCAAGCTTTGTGGA 1080  
DB 1021 CATCGAGCTCTGATCTCTCCAGTACAGGAGCAGCTGGAAAAAGTCCCAAGCTTTGTGGA 1080  
QY 1081 GACCCGCATCCAGTCTCCGTGATGAGCCCGGAGGGGCTACCTCTCAAGTGCCCAAGA 1140  
DB 1081 GACCCGCATCCAGTCTCCGTGATGAGCCCGGAGGGGCTACCTCTCAAGTGCCCAAGA 1140  
QY 1141 GCTCATCAAGACATTTGTAGAACCTTCCAAGGGCTGCCAGCTGGGGAAGACAGACAAAG 1200  
DB 1141 GCTCATCAAGACATTTGTAGAACCTTCCAAGGGCTGCCAGCTGGGGAAGACAGACAAAG 1200

QY 1201 CTTTGAGAACATGGACTACTTTTACTCTGGACTTAGAACACATAGCAGAGGCTTTGAGGGC 1260  
DB 1201 CTTTGAGAACATGGACTACTTTTACTCTGGACTTAGAACACATAGCAGAGGCTTTGAGGGC 1260  
QY 1261 CATTGACTTTGGGACAGTAAAGATGTGATTACATGTTTACCTTTGAAAGGCAGCG 1320  
DB 1261 CATTGACTTTGGGACAGTAAAGATGTGATTACATGTTTACCTTTGAAAGGCAGCG 1320  
QY 1321 TTCCTCTTGAGTTCTGAGGGGAACTGTTAAAAAAGTCAAAATTTACACAGCCAGTGTGAC 1380  
DB 1321 TTCCTCTTGAGTTCTGAGGGGAACTGTTAAAAAAGTCAAAATTTACACAGCCAGTGTGAC 1380  
QY 1381 AGGTCTCTATGAGAGCCCTGACTGTCTTAGTAGTGTCTAAGTAGACCAAGCTGTCTGG 1440  
DB 1381 AGGTCTCTATGAGAGCCCTGACTGTCTTAGTAGTGTCTAAGTAGACCAAGCTGTCTGG 1440  
QY 1441 AACACATAGAGATCTATCTGCCCATCTCTCTCTTGAGGGATGAGATAAAGGCATGT 1500  
DB 1441 AACACATAGAGATCTATCTGCCCATCTCTCTCTTGAGGGATGAGATAAAGGCATGT 1500  
QY 1501 GCCCACCATGCTCGCTCCACAGACAACTTTTGTGATGGATCCAGGTCTGGCACAGTCCC 1560  
DB 1501 GCCCACCATGCTCGCTCCACAGACAACTTTTGTGATGGATCCAGGTCTGGCACAGTCCC 1560  
QY 1561 TGGTACATAATTTGTTTGGAAATAAATTTATCTCGTGCC 1597  
DB 1561 TGGTACATAATTTGTTTGGAAATAAATTTATCTCGTGCC 1597

RESULT 3

US-10-775-627-5  
; Sequence 5, Application US/10775627  
; Publication No. US2004014246A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSON, ERIC  
; APPLICANT: SPENCER, JEFFREY A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
; FILE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS  
; FILE REFERENCE: MYOG:028USD1  
; CURRENT APPLICATION NUMBER: US/10/775,627  
; CURRENT FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 09/908,988  
; PRIOR FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/219,020  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1597  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (299)..(1327)  
US-10-775-627-5

Query Match 100.0%; Score 1597; DB 19; Length 1597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCGAGATTACCTTTACAGAACTGTTCCGGAGCACCTTCCCTTGGCAGCACACTCAG 60  
DB 1 CTCGAGATTACCTTTACAGAACTGTTCCGGAGCACCTTCCCTTGGCAGCACACTCAG 60  
QY 61 GCAGAGGACCGGCAAGGAATGACACTCTCTGAATACAACTTCTTCCAAAGACA 120  
DB 61 GCAGAGGACCGGCAAGGAATGACACTCTCTGAATACAACTTCTTCCAAAGACA 120  
QY 121 GCAGACCATGGAATACTTGGAAAAAGCAACTGATCTGTCCCCTCTGCCTAGAGATGTTTAC 180  
DB 121 GCAGACCATGGAATACTTGGAAAAAGCAACTGATCTGTCCCCTCTGCCTAGAGATGTTTAC 180  
QY 181 GAAGCCTGTGTCATTTCTCCCTTGGCCAGCAAACTGTGTGAGGAAATGTGGGGCCCCCCC 240



Db	181	GAAGCCTGTGGTCAATCTCCCTTGCAGCAACAACCTGTGCAGGAATGTGGGGCCCCC	240
Qy	241	TTGGAGCAAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTGCATTTCAAAGCAATAT	300
Db	241	TTGGAGCAAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTGCATTTCAAAGCAATAT	300
Qy	301	GGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGGAGAACTGTGAGAAAGCAGCT	360
Db	301	GGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGGAGAACTGTGAGAAAGCAGCT	360
Qy	361	GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCCTGTGGTCAATCCTGCTGCCAACA	420
Db	361	GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCCTGTGGTCAATCCTGCTGCCAACA	420
Qy	421	CAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGCCAA	480
Db	421	CAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGCCAA	480
Qy	481	CCGCGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTGCCGCCATGA	540
Db	481	CCGCGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTGCCGCCATGA	540
Qy	541	AGTGATCATGACCGGCACGGGGTGTAACGGCTGACAGAGAACTCTGCTGGTGGAAAAAT	600
Db	541	AGTGATCATGACCGGCACGGGGTGTAACGGCTGACAGAGAACTCTGCTGGTGGAAAAAT	600
Qy	601	CATTGACATCTACAGCAGAGTGTCTCCAGTCCGCGCTGCAGAAAGGACGCCACCGAT	660
Db	601	CATTGACATCTACAGCAGAGTGTCTCCAGTCCGCGCTGCAGAAAGGACGCCACCGAT	660
Qy	661	GTCAAGGAAACAGAGACAGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCTAC	720
Db	661	GTCAAGGAAACAGAGACAGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCTAC	720
Qy	721	TTGCTCCTTGTGCAAGGTGTTGGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAAG	780
Db	721	TTGCTCCTTGTGCAAGGTGTTGGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAAG	780
Qy	781	CATCTTCCAGGACAGAGACTGAGTGAATCTGCTCACTGCTCACGTGTGAGTGCCTAC	840
Db	781	CATCTTCCAGGACAGAGACTGAGTGAATCTGCTCACTGCTCACGTGTGAGTGCCTAC	840
Qy	841	CGACCGAGTGCAGACCATCATCTCTCAGCTGGAGGACTCGTGACAGAGTGAACAGAGAA	900
Db	841	CGACCGAGTGCAGACCATCATCTCTCAGCTGGAGGACTCGTGACAGAGTGAACAGAGAA	900
Qy	901	TAGCCACCAAGGTGAAGAGGAGCTGAGTCAAGAGTTTGACACCCCTTACGCCCATCTTGA	960
Db	901	TAGCCACCAAGGTGAAGAGGAGCTGAGTCAAGAGTTTGACACCCCTTACGCCCATCTTGA	960
Qy	961	TGAGAGAGAGAGAGCTGCTGAGCGGATCACGACGAGGACGAGGAGAGAGTGGGCTT	1020
Db	961	TGAGAGAGAGAGAGCTGCTGAGCGGATCACGACGAGGACGAGGAGAGAGTGGGCTT	1020
Qy	1021	CATCGAGGCTCTGATCCTCCAGTACAGGAGAGCTGGAAGTCCCAAGCTTGTGGA	1080
Db	1021	CATCGAGGCTCTGATCCTCCAGTACAGGAGAGCTGGAAGTCCCAAGCTTGTGGA	1080
Qy	1081	GACCGCATCCAGTCTGATGAGCCCGAGGGGTACCTTCTCTCAAGTGCACAGCA	1140
Db	1081	GACCGCATCCAGTCTGATGAGCCCGAGGGGTACCTTCTCTCAAGTGCACAGCA	1140
Qy	1141	GCTCATCAGAGACTTGTAGAAGCTTCCAGGGCTCCAGGCTGGGAGACAGAGCAAG	1200
Db	1141	GCTCATCAGAGACTTGTAGAAGCTTCCAGGGCTCCAGGCTGGGAGACAGAGCAAG	1200
Qy	1201	CTTTGAGAAATCGACTACTTTTACTCTGACTTTAGAACATACATAGCAGAGCCCTTGAGGC	1260
Db	1201	CTTTGAGAAATCGACTACTTTTACTCTGACTTTAGAACATACATAGCAGAGCCCTTGAGGC	1260
Qy	1261	CATTGACTTTGGACAGGTAAAGGATGTGATGTTTACATGTTTGAACCTTTGAAGGACGG	1320
Db	1261	CATTGACTTTGGACAGGTAAAGGATGTGATGTTTACATGTTTGAACCTTTGAAGGACGG	1320

Db	1261	CATTGACTTTGGACAGAGTAAAGGATGTGATGTTTACATGTTTGAACCTTTGAAGGACGG	1320
Qy	1321	TTCTCTTTCAGTCTCTGAGGGAACTGTTTAAAAAGTCAAAATTTACACAGCCAGTGTGAC	1380
Db	1321	TTCTCTTTCAGTCTCTGAGGGAACTGTTTAAAAAGTCAAAATTTACACAGCCAGTGTGAC	1380
Qy	1381	AGGTCTCTCTATGAGGCCCTGACTGTTTGTAGTAGTCTCTAAGTAGACCAAGCTGGTCTGG	1440
Db	1381	AGGTCTCTCTATGAGGCCCTGACTGTTTGTAGTAGTCTCTAAGTAGACCAAGCTGGTCTGG	1440
Qy	1441	AACACATAGAGATCTATCTTTGCCCATCTCTGTTCTTTGAGGGATGAGATAAAGGATGT	1500
Db	1441	AACACATAGAGATCTATCTTTGCCCATCTCTGTTCTTTGAGGGATGAGATAAAGGATGT	1500
Qy	1501	GCCCCACATGCTGCTCCACAGACAACTTTGTGATGATCCAGGCTCTGGCACAGTGC	1560
Db	1501	GCCCCACATGCTGCTCCACAGACAACTTTGTGATGATCCAGGCTCTGGCACAGTGC	1560
Qy	1561	TGGTACATTAATGTTTTCGAAATAAATTAATCTCGTGCC	1597
Db	1561	TGGTACATTAATGTTTTCGAAATAAATTAATCTCGTGCC	1597

RESULT 4

US-10-061-043A-20  
; Sequence 20, Application US/10061043A  
; Publication No. US20030129686A1  
; GENERAL INFORMATION:  
; APPLICANT: Glass, David  
; APPLICANT: Bodine, Sue  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES  
; FILE REFERENCE: REG 753B  
; CURRENT APPLICATION NUMBER: US/10/061, 043A  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: 60/338, 742  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/311, 697  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/264, 926  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 1053  
; TYPE: DNA  
; ORGANISM: rat  
US-10-061-043A-20

Query Match		55.8%	Score 890.8	DB 15	Length 1053
Best Local Similarity		93.3%	Pred. No. 7.7e-272		
Matches	931	Conservative	0	Mismatches	67
				Indels	0
				Gaps	0
Qy	299	ATGGATTATAAATCTAGCCCTGATTCCTGTATGGAACGCTATGGAGAACCTGGAGAACGAG	358		
Db	1	ATGGATTATAAATCTAGCCCTGATTCCTGGACGGAAATGCTATGGAGAACCTGGAGAACGAG	60		
Qy	359	CTGATCTGCCCATCTGCTCGGAGATGTTTACCAAGCTGTGTCTATCTGCCCTGCCAA	418		
Db	61	CTATCTGCCCATCTGCTCGGAGTGTACCAAGCTGTGTCTATCTGCCCTGCCAG	120		
Qy	419	CACAACTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTCGAAC	478		
Db	121	CACAACTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTCGAAC	180		
Qy	479	AACCGCGTGGCTCAGTGTCCATGTCTGAGGTGCTTTCCGTTGCCCTCGTCCGCCAT	538		
Db	181	AACCGCGTGGCTCAGTGTCCATGTCTGAGGTGCTTTCCGTTGCCCTCGTCCGCCAT	240		
Qy	539	GAAGTGATCATGGACCGGCACGGGTGTACGGCTCTCAGAGGAACCTGTGTGGGAAAC	598		
Db	241	GAAGTGATCATGGACCGGCATGCGGTGTACGGTGTGACAGAGNAACCTGTGTGGAGAAC	300		
Qy	599	ATCATTGACATCTACAAAGCAGGAGTGTCTCCAGTCCGCGCCCTCGCAAGAGGACCCCG	658		



Db 301 ATCATCGACATCTAAGCAGGAATGCTCCAGTCGGCCCTCGAAGAGGCGACCCCG 360  
Qy 659 ATGTGCAAGGAACAGGAAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCT 718  
Db 361 ATGTGCAAGGAACAGGAAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCT 420  
Qy 719 ACTTGCTCTTGTGCAAGGTGTTGGGCTACCAAGGCTGTGAGGTGCTTGTGCA 778  
Db 421 ACTTGCTCTTGTGCAAGGTGTTGGGCTACCAAGGCTGTGAGGTGCTTGTGCA 480  
Qy 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTGATCTCCATCTGCTGTGCGGG 838  
Db 481 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTGATCTCCATCTGCTGTGCGGG 540  
Qy 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGAGAGTGACCAAGGAG 898  
Db 541 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGAGAGTGACCAAGGAG 600  
Qy 899 AATAGCCACCGAGTGAAGGAGGAGTGAATCAAGATTTGACACCTCTACGCCATCTCG 958  
Db 601 AACGACCGAGTGAAGGAGGAGTGAATCAAGATTTGACACCTCTACGCCATCTCG 660  
Qy 959 GATGAGAGAGAGCGAGTCTGTCAGCGGATCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1018  
Db 661 GACGAGAGAGAGGAGTCTGTCAGCGGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Qy 1019 TTCTATCGAGGCTCTGATCTCTCAGTACAGGAGGAGTGAAGATTTGACCAAGCTTGTG 1078  
Db 721 TTCTATCGAGGCTCTGATCTCTCAGTACAGGAGGAGTGAAGATTTGACCAAGCTTGTG 780  
Qy 1079 GAGACCGGATCCAGTCTCGATGAGCGCGGAGGAGTCTCTCTCTCAAGTCCCAAG 1138  
Db 781 GAAACAGGATCCAGTCTCGATGAGCGCGGAGGAGTCTCTCTCTCAAGTCCCAAG 840  
Qy 1139 CAGCTCATCAGAGCATTTAGAGGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1198  
Db 841 CGCTCATCAGAGCATTTAGAGGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
Qy 1199 GCTTTGAGACATCGACTACTTTACTCTGGACTTTAGAACATATAGACATATAGACATATAG 1258  
Db 901 GCTTTGAGACATCGACTACTTTACTCTGGACTTTAGAACATATAGACATATAGACATATAG 960  
Qy 1259 GCCATTGACTTTGGACAGGTAAAGGATGTGATTTAC 1296  
Db 961 GCCATCGACTTTGGACAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 998

RESULT 5

US-10-060-634C-20  
; Sequence 20, Application US/10060634C  
; Publication No. US20030219739A1  
; GENERAL INFORMATION:  
; APPLICANT: Glass, David  
; APPLICANT: Bodine, Sue  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES  
; FILE REFERENCE: REG 753A  
; CURRENT APPLICATION NUMBER: US/10/060,634C  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: 60/338,742  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/311,697  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/264,926  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 1053  
; TYPE: DNA  
; ORGANISM: rat  
US-10-060-634C-20

Query Match 55.8%; Score 890.8; DB 17; Length 1053;  
Best Local Similarity 93.3%; Pred. No. 7,7e-272;  
Matches 931; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
Qy 299 ATGGATTAAATCTAGCCTGATTCCTGATGAAAGCGTATCGAGAACCTGAGAGAGCAG 358  
Db 1 ATGGATTAAATCTAGCCTGATTCCTGATGAAAGCGTATCGAGAACCTGAGAGAGCAG 60  
Qy 359 CTGATCTGCCCATCTGCTGAGATGTTTACCAAGCCTGTGGTTCATCTCGCCCTGCCAA 418  
Db 61 CTATCTGCCCATCTGCTGAGATGTTTACCAAGCCTGTGGTTCATCTCGCCCTGCCAG 120  
Qy 419 CACAACTCTGCGGAAAGTGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGACC 478  
Db 121 CACAACTCTGCGGAAAGTGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTGAGACC 180  
Qy 479 AACCGCGTGGCTCAGTCTCATGTCGAGGTCGTTCCGTTGCCCTCGTCGCCCAT 538  
Db 181 AACCGCGTGGCTCAGTCTCATGTCGAGGTCGTTCCGTTGCCCTCGTCGCCCAT 240  
Qy 539 GAAAGTATCATGGAACCGGCAAGGCTGTACGCGCTGCAGAGGAACCTGCTGTGGAAGAAC 598  
Db 241 GAAAGTATCATGGAACCGGCAAGGCTGTACGCGCTGCAGAGGAACCTGCTGTGGAAGAAC 300  
Qy 599 ATCATTTGACATCTCAAGCAGGAGTGTCCAGTCCGCGCTTGCAGAAAGGAGCAGCCCG 658  
Db 301 ATCATCGACATCTCAAGCAGGAAATGCTCCAGTCCGCGCTTGCAGAAAGGAGCAGCCCG 360  
Qy 659 ATGTGCAAGGAGACAGAGAGAGAGATCAACATCTACTGTCTCAGCTGAGGAGGCTCT 718  
Db 361 ATGTGCAAGGAGACAGAGAGAGAGATCAACATCTACTGTCTCAGCTGAGGAGGCTCT 420  
Qy 719 ACTTGCTCTTGTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGGTGCTGCCCTTTGCAA 778  
Db 421 ACTTGCTCTTGTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGGTGCTGCCCTTTGCAA 480  
Qy 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTGCAATCTCCTATGCTGTGCGGG 838  
Db 481 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTGCAATCTCCTATGCTGTGCGGG 540  
Qy 839 AACGACCGAGTGAAGGAGGAGTCTCAGCTGGAGGAGTCTGTCAGAGTGAAGGAGGAG 898  
Db 541 AACGACCGAGTGAAGGAGGAGTCTCAGCTGGAGGAGTCTGTCGAGTGAAGGAGGAGGAG 600  
Qy 899 AATAGCCACCGAGTGAAGGAGGAGTCTCAGCTGGAGGAGTCTGACACCTCTTACGCCATCT 958  
Db 601 AATAGCCACCGAGTGAAGGAGGAGTCTCAGCTGGAGGAGTCTGACACCTCTTACGCCATCT 660  
Qy 959 GATGAGAGAGAGCGAGTCTGTCAGCGGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1018  
Db 661 GATGAGAGAGAGCGAGTCTGTCAGCGGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Qy 1019 TTCTATCGAGGCTCTGATCTCTCAGTACAGGAGGAGTGAAGATTTGACCAAGCTTGTG 1078  
Db 721 TTCTATCGAGGCTCTGATCTCTCAGTACAGGAGGAGTGAAGATTTGACCAAGCTTGTG 780  
Qy 1079 GAGACCGGATCCAGTCTCGATGAGCGCGGAGGAGTCTCTCTCTCAAGTCCCAAG 1138  
Db 781 GAAACAGGATCCAGTCTCGATGAGCGCGGAGGAGTCTCTCTCTCAAGTCCCAAG 840  
Qy 1139 CAGCTCATCAGAGCATTTAGAGGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1198  
Db 841 CGCTCATCAGAGCATTTAGAGGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
Qy 1199 GCTTTGAGACATCGACTACTTTACTCTGGACTTTAGAACATATAGACATATAGACATATAG 1258  
Db 901 GCTTTGAGACATCGACTACTTTACTCTGGACTTTAGAACATATAGACATATAGACATATAG 960  
Qy 1259 GCCATTGACTTTGGACAGGTAAAGGATGTGATTTAC 1296  
Db 961 GCCATCGACTTTGGACAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 998



QY 502 GTCTGAGGTCTTTCCGTTGCTCCCTCGTGGCCCATGAGTGATCATGGACCGCACGG 561  
DB 639 GTCTGAGGCCGTTTCCGCTGCCCACTGCCGCCACGAGGTGATCATGGATCGTCACGG 698  
QY 562 GTGTACGCCCTGCAGAGAACCTCTGTTGGAAACATCATTTGACATCTCAACGACGA 621  
DB 699 AGTGTACGCCCTGCAGAGAACCTCTGTTGGAAACATCATTTGACATCTCAACGACGA 758  
QY 622 GTGCTCCAGTCCGCCCTGCAGAAAGGACGACCCGATGTGCAAGGAACACGAAAGAGA 681  
DB 759 GTGCTCCAGTCCGCCCTGCAGAGGCCAGTCAACCCCATGTGCAAGGACGACGAGATGA 818  
QY 682 GAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGT 741  
DB 819 GAAATCAACATCTACTGTCTCACTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGT 878  
QY 742 TGGGCTCACCAGGCTGTGAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCT 801  
DB 879 TGGGATCCACAGGCTGTGAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCT 938  
QY 802 TGAGTGTAGTAACTACTGTCTCACTGTGAGGTGCTTACTTGTGCAAGGTGCTTACT 861  
DB 939 TGAATGTAGTAACTACTGTCTCACTGTGAGGTGCTTACTTGTGCAAGGTGCTTACT 998  
QY 862 TTCTCAGTGTGAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCTTACTTGT 921  
DB 999 CACTCAGTGTGAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCTTACTTGT 1058  
QY 922 GCTGAGTCAAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCTTACTTGT 981  
DB 1059 GCTGAGCCAGAGTGTGCAAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCT 1118  
QY 982 GCAGCGGATCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1041  
DB 1119 GCAGCGGATCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1178  
QY 1042 GTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1101  
DB 1179 GTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1238  
QY 1102 TGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1161  
DB 1239 CGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1298  
QY 1162 AGCCTCCAAGGCTGCGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1221  
DB 1299 AGCTTCCAAGGCTGCGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1358  
QY 1222 TACTCTGGAATTAGAACACATAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1281  
DB 1359 TACTTTGGATTTAGAGCACATAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1418  
QY 1282 AGGATGTGATG 1292  
DB 1419 GGAAGAGGAAG 1429

RESULT 8  
US-10-221-625-192  
; Sequence 192, Application US/10221625  
; Publication No. US20040033942A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: HILMAN, Jennifer L.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: LU, Dying Aina M.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: TANG, Y. Tom

; APPLICANT: MATHUR, Preete  
; APPLICANT: SHAH, Purvi  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: REDDY, Roopa  
; TITLE OF INVENTION: TRANSCRIPTION FACTORS  
; FILE REFERENCE: PF-0761 PCT  
; CURRENT APPLICATION NUMBER: US/10/221,625  
; NUMBER OF SEQ ID NOS: 214  
; SOFTWARE: PERL Program  
; SEQ ID NO 192  
; LENGTH: 1764  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040033942A1 3575519CB1  
US-10-221-625-192

Query Match 50.2%; Score 802.2; DB 18; Length 1764;  
Best Local Similarity 86.1%; Pred. No. 1.5e-243;  
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;  
QY 262 GACGAGGTGGCAGAGACAGTCGCATTTCAAAGCAATATGGATTATAATCTAGCCTGAT 321  
DB 86 GAGGAGCTAGCGGTGGCTCTCATTTCTCCACAGAATGGATTATAAGTCGAGCCTGAT 145  
QY 322 TCCTGATGAAACGCTATGGAGAACCTGGAGAACGAGCTGATCTGCCCCATCTGCCCTGA 381  
DB 146 CCAGATGGGAATCCATGGAGAACTTGGAGAACGAGCTGATCTGCCCTATCTGCTCTGA 205  
QY 382 GATGTTTACCAGGCTGTGGTCACTCTGCCCTGCCAACACAACTCTGCCGGAAGTGTGC 441  
DB 206 GATGTTTACCAGGCTGTGGTCACTCTGCCCTGCCAACACAACTCTGCCGGAAGTGTGC 265  
QY 442 CAACGACATCTTCCAGGCTGCGAATCCCTACTGAGACCAACCGCGTGGCTCAGTGTCCAT 501  
DB 266 CAATGACATCTTCCAGGCTGCAAAATCCCTACTGAGACCAACCGCGGAGCTCAGTGTCCAT 325  
QY 502 GTCTGAGGTGTTTCCGTTGCTGCGCCCATGAAGTGATCATGGACCGGACCGCACGG 561  
DB 326 GTCTGAGGCCGTTTCCGCTGCCCACTGCGCCCAAGAGGTGATCATGGATCGTCACGG 385  
QY 562 GGTGTACGCGCTGCAGAGAACTCTGCTGGTGAACAACTATTGTGACATCTCAAGCAGA 621  
DB 386 AGTGTACGCGCTGCAGAGAACTCTGCTGGTGAACAACTCATCGACATCTCAAAACAGA 445  
QY 622 GTGCTCCAGTCCGCCCTGCAGAAAGGACGACCCGATGTGCAAGGAACACGAGACGA 681  
DB 446 GTGCTCCAGTCCGCCCTGCAGAAAGGAGTCAACCCCATGTGCAAGGAGCAGAAAGATGA 505  
QY 682 GAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGT 741  
DB 506 GAAATCAACATCTACTGTCTCACTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGT 565  
QY 742 TGGGCTCACCAGGCTGTGAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCTTACT 801  
DB 566 TGGGATCCACAGGCTGTGAGGTGCTTGTGCAAGGTGCTTACTTGTGCAAGGTGCTTACT 625  
QY 802 TGAGTGTAGTAACTACTGTCTCACTGTGAGGTGCTTACTTGTGCAAGGTGCTTACT 861  
DB 626 TGAATGAATAACTACTGTCTCACTGTGAGGTGCTTACTTGTGCAAGGTGCTTACT 685  
QY 862 CTCTCAGCTGGAGGACTCTGTGAGAGTGAACCAAGGAGAAATAGCCACAGGTGAAGGAGA 921  
DB 686 CACTCAGCTGGAGGATTTCCGTCGAGTGAACCAAGGAGAAACAGTCAACAGGTAAAGGAGA 745  
QY 922 GCTGAGTCAGAGTTTGAACACCTCTTACGCCATCTCTGGATGAGAAAGAGAGAGTGTCT 981  
DB 746 GCTGAGCCAGAGTTTGAACACCTCTTACGCCATCTCTGGATGAGAAAGAGTGTCT 805  
QY 982 GCAGCGGATCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1041

Db 806 GCAGCGGATCACGAGGAGCAGGAGAAAAGCTTAGCTTCATCGAGCCCTCATCCAGCA 865  
 QY 1042 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA 1101  
 Db 866 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA 925  
 QY 1102 TGAGCCGGAGGGGCTACCTTCTCTCAAGTGCACAAGCAGCTCATCAAGAGCATTTGAGA 1161  
 Db 926 CGAGCCTGGGGAGCCACCTTCTCTTGTAGTGCACAAGCAACTCATCAAAAGCATTTGGA 985  
 QY 1162 AGCCTCAAGGGTGCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAAATGAGACTACTT 1221  
 Db 986 AGCTTCAAGGGTGCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAAATGAGACTACTT 1045  
 QY 1222 TACTCTGGACTTAGAACACATACAGAGCCTTGGGGCCATTTGAGGACAGTAA 1281  
 Db 1046 TACTTTGGATTTAGAGCACATAGACGCGCTTGAGAGCAATTTGTTGGGACAGATGA 1105  
 QY 1282 AGGATGTGATG 1292  
 Db 1106 GGAAGAGGAAG 1116

RESULT 9

US-10-723-860-7801  
 ; Sequence 7801, Application US/10723860  
 ; Publication No. US20040253606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Ginsburg, Wendy M.  
 ; APPLICANT: Zlotnik, Albert  
 ; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &  
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
 ; FILE REFERENCE: 05882.0193.NPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/723,860  
 ; CURRENT FILING DATE: 2003-11-26  
 ; PRIOR APPLICATION NUMBER: 60/429,739  
 ; PRIOR FILING DATE: 2002-11-26  
 ; NUMBER OF SEQ ID NOS: 8393  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 7801  
 ; LENGTH: 2700  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-723-860-7801

Query Match 50.2%; Score 802.2; DB 20; Length 2700;  
 Best Local Similarity 86.1%; Pred. No. 1.8e-243;  
 Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;  
 QY 262 GACGCGAGTGGGCAAGACAGATCGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321  
 Db 992 GAGCGAGCTAGGGCTGGCTCTATTCCTCCCAAGAAATGGATTAAAGTCGAGCCTGAT 1051  
 QY 322 TCCTGATGGAACCGCTATGAGAACCTGGAGAACGAGCTGATCTGCCCCATCTGCCCTGGA 381  
 Db 1052 CCAGGATGGAATCCCATGAGAACTTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGGA 1111  
 QY 382 GATGTTTACCAAGCCTGTGTCTATCTGCCCTGCCAACCAACCTCTGCCGGAAGTGTGC 441  
 Db 1112 GATGTTTACCAAGCCTGTGTCTATCTGCCCTGCCAACCAACCTCTGCCGGAAGTGTGC 1171  
 QY 442 CAACGACATCTCCAGGCTGCGAATCCCTACTGAGCAACCGCGGTGGCTCAGTGTCCAT 501  
 Db 1172 CAATGACATCTCCAGGCTGCGAATCCCTACTGAGCAACCGCGGTGGCTCAGTGTCCAT 1231  
 QY 502 GTCTGGAGTGTCTTCCGTTGGCCCTCGTGGCCCATGAAGTATCATGACCGGACCGCAGCG 561  
 Db 1232 GTCTGGAGGCGGTTTCCGCTGCCCCACCTGCGCCACAGAGGTATCATGATCGTCACCG 1291  
 QY 562 GGTGTAGGGCTGCAGAGGACCTGCTGTGGGAAAACATCATTTGACATCTACAGCAGGA 621  
 Db 1292 AGTGTACGGCTGCAGAGGAACTGCTGTGGTGGAGAACATCATCGACATCTACAAACAGGA 1351

QY 622 GTGCTCCAGTCCGCCCCCTGCAGAAAAGGAGCCACCCGATGTGCAAGGAAACAGGAACGA 681  
 Db 1352 GTGCTCCAGTCCGCCCCCTGCAGAAAAGGAGCCACCCGATGTGCAAGGAAACAGGAACGA 1411  
 QY 682 GAAGATCAACTACTACTGTCTCACGTGTGAGGTGCTTACTTCTCTTGTGCAAGGTGTT 741  
 Db 1412 GAAATCAACTACTACTGTCTCACGTGTGAGGTGCTTACTTCTCTTGTGCAAGGTGTT 1471  
 QY 742 TGGGGCTCACAGGCTGTGAGGTGCTTGTGCCCCCTTGCNAAGCATCTTCCAGGACAGAGAC 801  
 Db 1472 TGGGATCCCAAGGCTGTGAGGTGCTTGTGCCCCCTTGCNAAGCATCTTCCAGGACAGAGAC 1531  
 QY 802 TGAGCTGAGTAACTTGCATCTCCATGCTGGTGGGGGAACCGAGTGCAGACGATCAT 861  
 Db 1532 TGAATGAATTAATGTATCTCCATGCTGGTGGGGGAATGACCGTGTGCAAGCATCAT 1591  
 QY 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGAGGAATAGCCACCGTGAAGGAGA 921  
 Db 1592 CACTCAGCTGGAGGATTTCCCGTCCAGTGACCAAGGAGAACAGTCAACAGGTAAGGAAGA 1651  
 QY 922 GCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTCGAGTGCAGAGGCTCTGATCCTCCA 1041  
 Db 1652 GCTGAGCCAGAAAGTTTGACACCGTTGTATGCCATCTCGAGTGCAGAAAGTGAAGTGTCT 1711  
 QY 982 GCAGCGGATCACGAGGAGCAGGAGGAGAAAGCTGGGCTTTCATCGAGGCTCTGATCCTCCA 1041  
 Db 1712 GCAGCGGATCACGAGGAGCAGGAGGAGAAAGTGTAGCTTTCATCGAGGCTCTGATCCTCCA 1771  
 QY 1042 GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA 1101  
 Db 1772 GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGAACTGCGCATCCAGTCCCTGGA 1831  
 QY 1102 TGAGCCGGAGGGGCTACCTTCTCTCAAGTGCAGAGCAGCTCATCAAGAGCATTTGAGA 1161  
 Db 1832 CGAGCCTGGGGAGGCGACCTTCTCTTGTACTGCCAAGCAACTCATCAAAAGCATTTGGA 1891  
 QY 1162 AGCCTCCAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTGTGAAACATGGACTACTT 1221  
 Db 1892 AGCTTCCAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTGTGAAACATGGACTACTT 1951  
 QY 1222 TACTCTGGACTTAGAACACATAGAGAGGCTTGTGAGGCGCATTTGGGACAGGTA 1281  
 Db 1952 TACTTTGGATTTAGAGCACATAGCAGCGCCCTGAGAGCCATTGACTTTGGGACAGATGA 2011  
 QY 1282 AGGATGTGATG 1292  
 Db 2012 GGAAGAGGAAG 2022

RESULT 10

US-10-094-749-1222  
 ; Sequence 1222, Application US/10094749  
 ; Publication No. US20030219741A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISOGAI, TAKAO  
 ; APPLICANT: SUGIYAMA, TOMOYASU  
 ; APPLICANT: OTSUKI, TETSUJI  
 ; APPLICANT: WAKAMATSU, AI  
 ; APPLICANT: SATO, HIROYUKI  
 ; APPLICANT: ISHII, SHIZUKO  
 ; APPLICANT: YAMAMOTO, JUN-ICHI  
 ; APPLICANT: ISONO, YUUKO  
 ; APPLICANT: HIO, YURI  
 ; APPLICANT: OTSUKA, KAORU  
 ; APPLICANT: NAGAI, KEIICHI  
 ; APPLICANT: IRIE, RYOTARO  
 ; APPLICANT: TAMECHIKA, ICHIRO  
 ; APPLICANT: SEKI, NAOHICO  
 ; APPLICANT: YOSHIKAWA, TSUTOMU  
 ; APPLICANT: OTSUKA, MOTOYUKI  
 ; APPLICANT: NAGAHARI, KENJI  
 ; APPLICANT: MASUHO, YASUHIKO

```
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1222
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1222

Query Match      50.1%; Score 800.6; DB 17; Length 1764;
Best Local Similarity 86.0%; Pred. No. 4.7e-243; Indels 0; Gaps 0;
Matches 887; Conservative 0; Mismatches 144;

QY 262 GACGAGGTGGGCAAGACAGTCGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 100 GAGGAGCTAGCGTGGCTCTATTCTTCCACAGATGGATTATAAGTCGAGCTGAT 159
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 TCCTGATGAAACGCTATGGAGAACTGTGAGAAAGCAGCTGATCTGCCCACTCTGCTGGA 381
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 160 CCAGGATGGAAATCCCATGGAGAACTTGAGAAAGCAGCTGATCTGCCCTATCTGCTGGA 219
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 382 GATGTTTACCAGCTGTGGTCTATCTCTCCCTGCCCAACACACACCTCTGCCGGAAGTGC 441
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 GATGTTTACCAGCAGTGGTCTATCTTCCGCTGCCAGCAGACAACTGTGCCGGAAGTGC 279
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 442 CAACGACATCTTCCAGGCTCGAAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 501
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 CAATGACATCTTCCAGGCTGCAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 339
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 GTCTGGAGTGTCTTCCGTTGCCCTCTGTCGCGCATGAAGTGATCATGGACCGCACGG 561
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 GTCTGGAGGCGCTTCCGCTGCCACCTGCGCCACGAGGTGATCATGGATCGTCAAGG 399
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 562 GGTGTACGCTGCGAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTACACAGCA 621
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 400 AGTTTACGCGCTGCAGAGAACTCTGCTGGAGAAACATCATCTGACATCTACAAACAG 459
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 622 GTGCTCCAGTCCGCGCTGCAGAAAGCAGCACCCGATGTGCAAGGAACACGAAAGCA 681
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 460 GTGCTCCAGTCCGCGCTGCAGAGGAGAGTCAACCCATGTGCAAGGACACGAAAGTA 519
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 682 GAAATCAACATCTACTGTCTCACGTGTGAGTGCCTACTTGTCTCTTGTGCAAGGTGT 741
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 520 GAAATCAACATCTACTGTCTCACGTGTGAGTGCCTACTTGTCTCTTGTGCAAGGTGT 579
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 TGGGCTCACGAGCTGTGAGTGTGCGCTTTCGAAAGCATCTTCCAAAGGACAGCAAG 801
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 580 TGGGATCCACAAAGGCTGCGAGGTGCGCCCATTTGCAGAGTGTCTTCCAGGGACAAAG 639
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 802 TGAGCTGAGTACTGTCTCATCTGCTGGTGGGGAACGACCGAGTGCAGACCATCAT 861
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 640 TGAATGAATACTGTATCTCATCTGCTGGTGGGGAATGACCGTGTGCAACCATCAT 699
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 862 CTCTCAGCTGGAGGACTCGTGAGAGTGACCAAGAGGAATAGCCACGAGGTGAAGGAG 921
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 700 CACTCAGCTGGAGGATTCGCTGAGTGACCAAGGAGAACAGTCAACGAGTAAAGGA 759
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 922 GCTGAGTCGAAGTTTGAACCCCTCTACGCCATCTCTGATGAGAGAGAGGAGCTGCT 981
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 760 GCTGAGCCAGAAAGTTTGAACCCCTCTATGCCATCTCTGATGAGAGAAAGTGAAGTGT 819
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 982 GCAGCGGATCACGAGGAGCAGGAGAGAGTGGCTTCTATCGAGGCTCTGATCCTCCA 1041
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 820 GCAGCGGATCACGAGGAGCAGGAGAGAGTGGCTTCTATCGAGGCTCTGATCCTCCA 879
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1042 GTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA 1101
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 502 GAAAAATAACATCTACTGTCTCTCAGTGTGAGGTGCCACCTGTCTCCATGTGTCAAGGTGTT 561  
QY 742 TGGGGCTCACACGCGCTGTGAGGTGCCCCCTTTGCAAAAGCATCTTCCAAAGGACAGAGAC 801  
Db 562 TGGGATCCAAAGGCTTGCAGGTGGCCCCATTGCAAGTGTCTTCCAGGGAACAAAGAC 621  
QY 802 TGAGCTGAGTAACATGTCATCTCCATGTGTGTGGGGGAACGACCGAGTGCAGACGATCAT 861  
Db 622 TGAACGAATAACATGTATCTCCATGTGTGTGGGGGAATGACCGTGTGCAGACCATCAT 681  
QY 862 CTCTAGCTGGAGGACTGTGTGAGAGTACCAAGGAGATAGCCACAGGTGAAGGAGGA 921  
Db 682 CACTCAGCTGGAGGATTTCCCGTCGAGTGACCAAGGAGAACAGTCAACAGGTAAAGGAAGA 741  
QY 922 GCTGAGTCAAGAGTTTGACACCTCTACGCGCATCTCGGATGAGAAGAGCGAGCTGCT 981  
Db 742 GCTGAGCCAGAGTTTGACACGTTGTATGCCATCTCGGATGAGAAGAAAGTGAAGTGTCT 801  
QY 982 GCAGCGGATCACGAGGAGCAGGAGGAGAGCTGGGCTTCATCGAGGCTCTGTATCTCTCA 1041  
Db 802 GCAGCGGATCACGAGGAGCAGGAGGAGAAAGCTTAGCTTCATCGAGGCTCTATCCAGCA 861  
QY 1042 GTACAGGAGCAGCTGAAAGTCCACCAAGCTTGTGGAGACCGGCATCCAGTCCCTGGA 1101  
Db 862 GTACAGGAGCAGCTGGACAAAGTCCACAAAGCTGTGGAACTGCCATCCAGTCCCTGGA 921  
QY 1102 TGAGCCGGAGGGGCTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATCTTGA 1161  
Db 922 CGAGCTTGGGGAGCCACCTTCTCTTGACTGCTCAAGCAACTCATCAAGAGCATCTTGA 981  
QY 1162 AGCTTCCAAGGGTGCAGCTGGGGAAGACAGAGCAAGGCTTTTGAGAACATGGACTACTT 1221  
Db 982 AGCTTCCAAGGGTGCAGCTGGGGAAGACAGAGCAGGCGCTTTTGAGAACATGGACTTCT 1041  
QY 1222 TACTCTGACTTAGACACATAGCAGAGGCTTGAGGGCCATTTGACTTTGGGACAGGTA 1281  
Db 1042 TACTTTGGATTTAGACACATAGCAGCGCCTTGAGAGCCATTTGACTTTGGGACAGATGA 1101  
QY 1282 AGGATGTGATG 1292  
Db 1102 GGAAGAGGAG 1112

RESULT 12

US-10-204-921-12

; Sequence 12, Application US/10204921

; Publication No. US2005009587A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: PANZER, Scott R.

; APPLICANT: SPIRO, Peter A.

; APPLICANT: BANVILLE, Steven C.

; APPLICANT: SHAH, Purvi

; APPLICANT: CHALUP, Michael S.

; APPLICANT: CHANG, Simon C.

; APPLICANT: CHEN, Alice

; APPLICANT: D'SA, Steven A.

; APPLICANT: AMSHEY, Stefan

; APPLICANT: DAHL, Christopher R.

; APPLICANT: DAM, Tam C.

; APPLICANT: DANIELS, Susan E.

; APPLICANT: DUFOUR, Gerard E.

; APPLICANT: FLORES, Vincent

; APPLICANT: FONG, Willy T.

; APPLICANT: GREENAWALT, Lila B.

; APPLICANT: HILLMAN, Jennifer L.

; APPLICANT: JONES, Anissa L.

; APPLICANT: LIU, Tommy F.

; APPLICANT: ROSEBERRY, Ann M.

; APPLICANT: ROSEN, Bruce H.

; APPLICANT: RUSSO, Frank D.

; APPLICANT: STOCKDREHER, Theresa K.

; APPLICANT: DAFFO, Abel

; APPLICANT: WRIGHT, Rachel J.  
; APPLICANT: YAP, Pierre E.  
; APPLICANT: YU, Jimmy Y.  
; APPLICANT: BRADLEY, Diana L.  
; APPLICANT: BRATCHER, Shawn R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: COHEN, Howard J.  
; APPLICANT: HODGSON, David M.  
; APPLICANT: LINCOLN, Stephen B.  
; APPLICANT: JACKSON, Stuart  
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT  
; FILE REFERENCE: PT-1133 PCT  
; CURRENT APPLICATION NUMBER: US/10/204,921  
; CURRENT FILING DATE: 2002-08-23  
; PRIOR APPLICATION NUMBER: 60/185,213; 60/205,285; 60/205,232; 60/205,323; 60/205,287;  
; 60/205,324; 60/205,286  
; PRIOR FILING DATE: 2000-02-24; 2000-05-17; 2000-05-16; 2000-05-17; 2000-05-17;  
; 2000-05-17; 2000-05-17  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PERL Program  
; SEQ ID NO 12  
; LENGTH: 2110  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: LG:247384.1:2000MAY19  
; US-10-204-921-12

Query Match 46.8%; Score 747.8; DB 21; Length 2110;  
Best Local Similarity 82.8%; Pred. No. 3.1e-226;  
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 262 GACGAGGTGGGCAAGACAGTCGCATTTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321  
Db 88 GAGGACGTAGCGTGGCTCTCATTCCTTCCACAGAATGGAATTAAGTCGAGCCTGAT 147  
QY 322 TCCTGATGAAACGGCTATGGAGAACCTGGAGAGAGCTGATCTGCCCATCTGCCCTGGA 381  
Db 148 CCAGNATGGATCCCATGGAGNACTTGGAGAGAGCTGATCTGCCCTATCTGCCCTGA 207  
QY 382 GATGTTTACCAAGCCTGTGTCATCTGCCCTTGCCTGCCAACACAACTCTGCCGGAAGTGTGC 441  
Db 208 GATGTTTACCAAGCAGTGTCTCATCTTCCGTGCCAGCAACAACCTGTGCCGGAAGTGTGC 267  
QY 442 CAACGACATCTTCCAGGCTGCCAATCCCTACTGGACCAACCGGCTGCTCAGTGTCCAT 501  
Db 268 CAATGATATTTTCCAGGCTCTTAACCCGTATTTGCCCAACAAGAGGAGGTACCACCATGGC 327  
QY 502 GTCTGGAGGTGCTTTTCCGTTCGCCCTCGTGCCTCATGAAGTGATCATGGACCGGCACGG 561  
Db 328 ATCAGGGGCGCATTCGGCTGCCCATCTCTGTAGACATGAAGTGGTTTGGATAGACATGG 387  
QY 562 GGTGTACGGCCTGCAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTTCAAGCAGGA 621  
Db 388 GGTATATGGACTTCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAACAGGA 447  
QY 622 GTGCTCCAGTCGGCCCCCTGCAGAAAGGACGCCACCGATGTGCAGGACACGAAAGACGA 681  
Db 448 GTGCTCCAGTCGGCGCGCTGCAGAAAGGCGAGTCACCCCATGTGCAAGGAGCAGCAAGATGA 507  
QY 682 GAAGATCAACATCTACTGTCTCACGTGTGAGGTGCCCTACTTGTCTCTTGTGCAAGGTGTT 741  
Db 508 GAAATCAACATCTACTGTCTCACGTGTGAGGTGCCACCTGCTCCATGTGCAAGGTGTT 567  
QY 742 TGGGGCTCACAGGCTGTGAGGTGCCCTTTGCAAGACATCTTCAAGGACAGAAAGAC 801  
Db 568 TGGGATCCCAAGGCGCTCGAGGTGGCCCCCATTTGCAGAGTGTCTTCCAGGGAACAAAGAC 627  
QY 802 TGAGCTGAGTAACTGCATCTCCATCTGCTGGTGGGGGACGACCGGAGTCACAGCATCAT 861  
Db 628 TGAACCTGAATAACTGTATCTCCATCTGCTGGTGGGGGAATGACCCGTGTGCAGACCATCAT 687

Qy	862	CTCTCAGCTGGAGGACTGTGTCAGAGTGA	CGAAGGAGAA	TAGCAC	CAGGTGAAGGAGGA	921
Db	688	CACTCAGCTGGAGGATTC	CCCGTCGAGTGA	CCCAAGGAGAA	CAGTCCACAGGTAAGGGAAGA	747
Qy	922	GCTGAGTCAGAACTTTGACACCCCTCTACGCCATCCTCGATGAGAAGAAAGACGAGCTGCT	981			
Db	748	GCTGAGCCAGAACTTTGACACGTTGTATGCCATCCTCGATGAGNAAGAAAGTGAAGTTGCT	807			
Qy	982	GCAGCGGATCA	CGCAGGACGAGGAGGAGAA	AGCTGGGCTT	CATCGAGGCTCTGATCTCTCCA	1041
Db	808	GCAGCGGATCACG	CAGGACGAGGAGAAAAAGCTTAGCTT	CATCGAGGCCCTCATCCACGA	867	
Qy	1042	GTACAGGGACAGCTGCAAAAGTCCACCAAGCTGTGTGAGACCGCCATCCAGTCCCTGGA	1101			
Db	868	GTACCGAGGACAGCTGGAACAAGTCCACAAAGCTGGTGAAC	TGCCATCAGTCCCTCGGA	927		
Qy	1102	TGAGCCCGAGGGGCTACCTTCTCTCAAGTGCCAAAGCAGCTCATCAAGAGCATTTGTAGA	1161			
Db	928	CGAGCCTGGGGAGCCACCTTCTCTTGACTGCCCAAGCAACTCATCAAAAGCATTTGTGGA	987			
Qy	1162	AGCTTCAAGGGCTGCCAGCTGGGGGAGACAGACCAAGGCTTTGAGAAACATGCACTACTT	1221			
Db	988	AGCTTCAAGGGCTGCCAGCTGGGGGAGACAGACAGGGGCTTTGAGAAACATGGACTTCTT	1047			
Qy	1222	TACTCTGGACTTTAGAA	CACATAGCAGAGGGCCTTGAGGGCCATTGACTTTTGGGACAGGTAA	1281		
Db	1048	TACTTTGGATTTAGAGCACATAG	CACAGCGCCCTGAGAGCCATTGACTTTTGGACAGATGA	1107		
Qy	1282	AGGATGTGATG	1292			
Db	1108	GGAAAGAGGAAG	1118			

RESULT 13

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US-10-061-043A-32
; Sequence 32, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 32
; LENGTH: 630
; TYPE: DNA
; ORGANISM: rat
US-10-061-043A-32

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	Query Match	34.3%	Score 547.4;	DB 15;	Length 630;
	Best Local Similarity	94.0%;	Pred. No. 8.6e-163;		
	Matches 569;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;
Qy	295	CAATATGAGTTTATAAATTCTAGCCTGGATTTCCTGATGGAAAACGCTATGAGAACCTGGAGAA	354		
Dd	21	CGACAAGAATTATAAATCTGGCTTGATTCGGACGGAAATGCTATGAGAACCTGGAGAA	80		
Qy	355	GCAGCTGATCTGTGCCCATCTGCCTGGAGATGTTTTACCAAGCCTGTGGTTCATCTCGCCCTG	414		
Dd	81	GCAGCTCATCTGCCCCACTCTGSCCTTGAGATGTTTTACC AAGCCTGTGGTTCATCTCGCCCTG	140		
Qy	415	CCACA CAACCTCTGCCGGAAGTGTGCCAACGCA CATCTTCAGGCTGCGAATCCCTACTG	474		
Dd	141	CCAGCAACACTCTGCCGGAAGTGTGCCAAGCATCTTCAGGCTGCGAATCCCTACTG	200		

Qy	475	GACCAACCGCGGTGGCTCAGTGTCCATGTCTGGAGGTCTGTTTCGGTTCGCCCTCTGTCGGC	534
Db	201	GACCAACCGCGGTGGCTCGGTGTCCATGTCTGGAGGTCTGTTTCGGCTCGCCCTCTGTCGGC	260
Qy	535	CCATGAAGTGTATCATGACCGGCACGGGGTCTACGGCCTGCAGAGAAACCTGCTGGTGA	594
Db	261	CCATGAAGTGTATCATGACCGGCATGGGGTGTACGGTCTGCAGAGAAACCTGCTGGTGA	320
Qy	595	AAACATCATTTGACATCTACAAAGCAGGAGTGTCTCAGTTCGGGCCCTGCAGAAAGGCAGCCA	654
Db	321	GAACATCATTCGACATCTACAAAGCAGGAATGTCTCCAGTCGGGCCCTGCAGAAAGGCAGCCA	380
Qy	655	CCCCATGTGCAAGGAACACGAAAGCAGAGACATCAACATCTACTGTCTTCACGTGTGAGGT	714
Db	381	CCCCATGTGCAAGGAACACGAAAGCAGAGAAATCAACATCTACTGTCTTCACGTGTGAGGT	440
Qy	715	GCCTACTTGTCTCTTGTGCAAGGTGTTTGGGGCTCACCAAGCCCTGTGAGGTTGCCCTTTT	774
Db	441	GCCTACTTGTCTCTTGTGCAAGGTGTTTGGGGCTCACCAAGCCCTGTGAAAGTTGCCCTTT	500
Qy	775	GCAAGACATCTTCCAAGGACAGAGAAGCTGAGCTGAGTAACTGCATCTCCATGCTGGTGGC	834
Db	501	ACAAGACATCTTCCAAGGACAGAGAAGCTGAACTGAGCAATTTGCACTCTCATGCTGGTGGC	560
Qy	835	GGGGAAACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTCGAGAGTCAACCA	894
Db	561	AGGGAAACGACCGAGTTCAGACTATCACTCGCAGCTGGAGGACTCTCTGCGAGTCAACCA	620
Qy	895	GGAGA	899
Db	621	GGTGA	625

## RESULT 14

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US-10-060-634C-32
; Sequence 32, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL METHOD FOR THE PREPARATION OF POLYMER-NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 630
; TYPE: DNA
; ORGANISM: rat
US-10-060-634C-32

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Query Match	34.3%	Score 547.4;	DB 17;	Length 630;
Best Local Similarity	94.0%;	Pred. No. 8.6e-163;		
Matches 569;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;
QY	295	CAATATGGATTATAAATCTAGCTGATTCCTGTATGGAAACGCTATGAGAACCTGGAGAA	354	
Db	21	CGACAAAGATTATAAATCTGCTGATTCCGACGGAAATGCTATGAGAACCTGGAGAA	80	
QY	355	GCAGCTGATCGCCCAATCTGCCCTGGAGATGTTTACCAAGCCTGTGTGTATCTCTGCCCTG	414	
Db	81	GCAGCTCATCTGCCCAATCTGCCCTGGAGATGTTTACCAAGCCTGTGTGTATCTCTGCCCTG	140	
QY	415	CCACACAAACCTCTGCCGGAAGTGTGCCAAGCATCTTCCAGGCTCGGAATCCCTACTG	474	



Db	141	CCAGCAACACCTCTGCGGGAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTG	200
QY	475	GACCAACCGGGTGGCTCAGTGTCCATGTCTGGAGTTCGTTTCGGCTTGGCCCTCGTGGCG	534
Db	201	GACCAACCGGGTGGCTCAGTGTCCATGTCTGGAGTTCGTTTCGGCTTGGCCCTCGTGGCG	260
QY	535	CCATGAAGTGCATGATGACCGGCAACCGGGGTGTACGGCTTGCAGAGGAACCTGCTGGTGA	594
Db	261	CCATGAAGTGCATGATGACCGGCAACCGGGGTGTACGGCTTGCAGAGGAACCTGCTGGTGA	320
QY	595	AAACATCATTTGACATCTAACAGCAGAGTGTCTCAGTGGCCCTTGCAGAAAGGAGCCCA	654
Db	321	GAACATCATTCAGATCTTACAGCAGGAATCTCAGTGGCCCTTGCAGAAAGGAGCCCA	380
QY	655	CCGATGTGCAAGGAACACGAAGCAGAGATCAACATCTACTGTCTCAGCGTGCAGGT	714
Db	381	CCGATGTGCAAGGAACACGAAGCAGAGATCAACATCTACTGTCTCAGCGTGCAGGT	440
QY	715	GCCTACTTGTCTCTGTGCAAGGTGTGTTGGGGCTCACCAAGGCTGTGAGGTTCGCCCTTT	774
Db	441	GCCTACTTGTCTCTGTGCAAGGTGTGTTGGGGCTCACCAAGGCTGTGAGGTTCGCCCTTT	500
QY	775	GCAAGCATCTTCCAGGACAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	834
Db	501	ACAAAGCATCTTCCAAAGGACAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	560
QY	835	GGGGAACGACGAGTGCAGACGATCTCTCAGCTGGAGGACTCGTGCAGAGTGAACCA	894
Db	561	AGGGAACGACGAGTGCAGACGATCTCTCAGCTGGAGGACTCGTGCAGAGTGAACCA	620
QY	895	GGAGA 899	
Db	621	GGTGA 625	

Db	346	TGTGCAACGACGCTCTTCCAGGCTCTAATCTCTCTGTGCAATCCCGGGCTCCACAACG	405
QY	497	TCCATGTCTGGAGTGTGTTTCGGTTCGCCCTCGTGGCGGCATGAAGTGAATCATGGACCG	556
Db	406	GTGTCTTCCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCTCTGGCAG	465
QY	557	CACGGGCTGTACGGCTCGCAGAGAACCTGCTGGTGGAAAAACATATTGACATCTCAACAG	616
Db	466	CATGTGTCTTAGCCCTCGCAGGGAACCTTGTAGTGGAGAACATATTGACATCTCAACAG	525
QY	617	CAGGAGTGTCTCCAG---TCGGGCCCTTGCAGAAAGGCGCACCCCGATGTCCAGGAACAC	673
Db	526	CAGGAGTGTCTCCCGGCCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC	585
QY	674	GAAGCAGAAAGTCAACATCTACTGTCTCAGTGTGAGGTGCTTACTTGTCTCTCTGTGC	733
Db	586	GAGGACGAGAAGTCAACATCTACTGTCTGAGTGTGAGGTGCTTGTCTCTCTCTCTCTGC	645
QY	734	AAGGTGTGTTGGGGCTCACCAAGGCTGTGAGGTGTGCCCTTTGCAAAAGCATCTTCCAAAGGA	793
Db	646	AAGGTGTGTTGGGGCTCACCAAGGCTGTGAGGTGTGCCCTTTGCAAAAGCATCTTCCAAAGCG	705
QY	794	CAGAAAGTGTGAGTGAATCTCCATCTCCATCTGCTGGTGGCGGGGAACGACCGAGTGCAG	853
Db	706	CAGAAAGTGTGAGTGAATCTCCATCTCCATCTGCTGGTGGCGGGGAACGACCGTGTGCAG	765
QY	854	ACGATCATCTCTCAGCTGAGGACTCGTGCAGAGTGAACCAAGGAGNATAGCCACCGAGTG	913
Db	766	GCAGTGTATCACCACGATGAGGAGGTGTGCCAGACCAATTGAGGACCAACAGCCGACAGAC	825
QY	914	AAGGAGGAGTGTGAGTGAATCTTACACCTCTTACGCCATCTGTGATGAGAAGAGAGC	973
Db	826	AAGCACTGTATAACAGAGGTTCGAGACCTGTGTGGCGGTTTGGAGGAGCGCAAGGGC	885
QY	974	GAGCTGTGCAGCGGATACGAGGAGGAGGAGAGAGTGGCTTCTCAAGTGCACAGCTCATCAAGAGC	1033
Db	886	GAACTGTCTCAAGCACTGGCCCGGAGCAGGAGGAGAGTGTGAGCGCTGTGGGGGCTC	945
QY	1034	ATCCTCCAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAG	1093
Db	946	ATCCGCGAGTACGAGAGACCACTTGGAGGGCTCTCTCAAGTGTGGTGGAGTCCGCAATCCAG	1005
QY	1094	TCCTGTGATGAGCCCGGAGGGCTACTTCTCTCAAGTGCACAGCTCATCAAGAGC	1153
Db	1006	TCCATGGAGAGCGCCAGATGCTCTTACTCTCCAGCAGCAAGAGAGTGTATCAACAG	1065
QY	1154	ATTGTAGAAGCTTCAAGGGCTGCCAGCTGGGGAGAGACAGCAAGGCTTTTGAGAACATG	1213
Db	1066	GTCCGGGCAATGTGAAAGTGTGAGCTGGCAGGACGGCCGAGCGAGGCTATGAGAGCATG	1125
QY	1214	GACTACTTACTCTGGACTTAGAACATAGCAGAGGCTTGGAGGCGCATTTGTTGGG	1273
Db	1126	GAGCAATCTCTGTGAGCGTGGAGCAGCGTGGCGGAAATGTGCGAACCATCGACTTCCAG	1185
QY	1274	ACAGGTAAAGGATGTGATG 1292	
Db	1186	CCGGGCGCGCTGGGGATG 1204	

RESULT 16  
US-10-775-649-1  
; Sequence 1, Application US/10775649  
; Publication No. US20040132160A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSON, ERIC  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS  
; FILE REFERENCE: MYOG:028USD2  
; CURRENT APPLICATION NUMBER: US/10/775,649  
; PRIOR FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 09/908,988

Query Match 30.3%; Score 484.6; DB 9; Length 1431;  
Best Local Similarity 69.2%; Pred. No. 1.2e-142;  
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;  
  
QY 317 CTGATTCCTGATGGAACGCTATGGAGAACCTTGGAGACGAGTGTATGCTGCCCCATCTGC 376  
Db 226 CTGCTAGGGATCGGCACACATGGAACACTTGGAGAGCAGTCAATTTGCCCATCTGC 285  
QY 377 CTGGAGATGTTTACCAAGCTGTGGTCACTCCTGCCCTGCCAACACAACTCTGCCGGAAG 436  
Db 286 CTGGAGATGTTTCCAAAGCCGCTGGTGAATCTTCCCTGCCACACAACTGTGCCGCAAG 345  
QY 437 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG 496



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; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-10-775-649-1

Query Match      30.3%; Score 484.6; DB 19; Length 1431;
Best Local Similarity 69.2%; Pred. No. 1.2e-142;
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 317 CTGATTCCTGATGGAAACGCTATGGAGAACCTGGAGAACGACGATCTGCCCCATCTGC 376
DB |||||
QY 226 CTGCTAGGGGATGGCAACAAATGGACAACTTGGAGAGCAGCTCATTTGCCCATCTGC 285
DB |||||
QY 377 CTGGAGATGTTTACCAAGCCTGTGTCTATCTCTGCGCCCTGCGCAACCAACAACTCTGCGGAG 436
DB |||||
QY 286 CTGGAGATGTTTCTCAAGCCGCTGTGTGATCTTGCCTGCGCAACCAACAACTGTGCGGCAAG 345
DB |||||
QY 437 TGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG 496
DB |||||
QY 346 TGTGCAACGACGCTTCTCCAGGCTTAACTCTCTGTGGCAATCCCGGGCTCCCAACAG 405
DB |||||
QY 497 TCCATGTCTGGAGGTCGTTTCCGTTGCGCCCTGCTGCGCCATGAAGTATCATGACACCG 556
DB |||||
QY 406 GTGTCTTCAAGAGGACGTTTCCGATGCCATCTTGTAGGACGAGTGTCTTGGACAGG 465
DB |||||
QY 557 CACGGGGTGTAGGGCTCTCAGAGGAACCTGTGTGGTGGAAACATCATTTGACATCTTCAAG 616
DB |||||
QY 466 CATGTGTCTATGGCTCTCAGCGGAACCTGCTAGTGGAGAACATCATTTGACATCTTCAAG 525
DB |||||
QY 617 CAGGAGTGCTCCAG---TCGGCCCTTGCAGAAAGCGACGCCATGTGCAAGGAACAC 673
DB |||||
QY 526 CAGGAGTCTCTCCGGCCACTGACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC 585
DB |||||
QY 674 GAAGACGAGAAATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTGTCTCTTGTGC 733
DB |||||
QY 586 GAGGACGAGAAATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTGTCTCTCTCTGC 645
DB |||||
QY 734 AAGGTGTTTGGGGCTCACCAGGCTGTGAGTGGCTTCCCTTTCGAAGCATCTTCCAAAGA 793
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QY 646 AAGGTGTTTGGGGCTCACCAGGCTGTGAGTGGCTTCCCTTTCGAAGCATCTTCCAAAGC 705
DB |||||
QY 794 CAGAAAGCTGAGTGAAGTAACTGCACTCTCCATGCTGGTGGCGGGGAAACGACCGAGTGCAG 853
DB |||||
QY 706 CAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 765
DB |||||
QY 854 ACGATCATCTCTCAGCTGGAGGACTGTGTCAGAGTGACCAAGGAGAAATAGCCACAGGTG 913
DB |||||
QY 766 GCAGTGATCACCAGATGAGGAGGAGTGTGCAGACCATTTAGGACAAACAGCCGACAGAC 825
DB |||||
QY 914 AAGGAGGAGCTGAGTCAAGAGTTTGAACACCTCTACGCCATCTGTGATGAGAGAGAGC 973
DB |||||
QY 826 AAGCAACTTTAAACCAAGAGGTTTCAAGACCTTGTGCGGGCTTGTGGAGGAGCGCAAGGGC 885
DB |||||
QY 974 GAGCTGCTCAGCGGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033
DB |||||
QY 886 GAATGCTTCAAGCACTGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
DB |||||
QY 1034 ATCTCTCAGTACGAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAG 1093
DB |||||
QY 946 ATCCGCCAGTACGAGACCACTTGGAGGCTCTCTCAAAGCTGTGTGAGTCCGCCATCCAG 1005
DB |||||
QY 1094 TCCCTGGATGACCGGAGGAGGAGTACCTTCTCTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAG 1153
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QY 1006 TCCATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1065
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RESULT 17
US-10-775-627-1
; Sequence 1, Application US/10775627
; Publication No. US20040142446A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-10-775-627-1
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Query Match      30.3%; Score 484.6; DB 19; Length 1431;
Best Local Similarity 69.2%; Pred. No. 1.2e-142;
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 317 CTGATTCCTGATGGAAACGCTATGGAGAACCTGGAGAACGACGATCTGCCCCATCTGC 376
DB |||||
QY 226 CTGCTAGGGGATGGCAACAAATGGACAACTTGGAGAGCAGCTCATTTGCCCATCTGC 285
DB |||||
QY 377 CTGGAGATGTTTACCAAGCCTGTGTCTATCTCTGCGCCCTGCGCAACCAACAACTCTGCGGAG 436
DB |||||
QY 286 CTGGAGATGTTTCTCAAGCCGCTGTGTGATCTTGCCTGCGCAACCAACAACTGTGCGGCAAG 345
DB |||||
QY 437 TGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG 496
DB |||||
QY 346 TGTGCAACGACGCTTCTCCAGGCTTAACTCTCTGTGGCAATCCCGGGCTCCCAACAG 405
DB |||||
QY 497 TCCATGTCTGGAGGTCGTTTCCGTTGCGCCCTGCTGCGCCATGAAGTATCATGACACCG 556
DB |||||
QY 406 GTGTCTTCAAGAGGACGTTTCCGATGCCATCTTGTAGGACGAGTGTCTTGGACAGG 465
DB |||||
QY 557 CACGGGGTGTAGGGCTCTCAGAGGAACCTGTGTGGTGGAAACATCATTTGACATCTTCAAG 616
DB |||||
QY 466 CATGTGTCTATGGCTCTCAGCGGAACCTGCTAGTGGAGAACATCATTTGACATCTTCAAG 525
DB |||||
QY 617 CAGGAGTGCTCCAG---TCGGCCCTTGCAGAAAGCGACGCCATGTGCAAGGAACAC 673
DB |||||
QY 526 CAGGAGTCTCTCCGGCCACTGACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC 585
DB |||||
QY 674 GAAGACGAGAAATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTGTCTCTTGTGC 733
DB |||||
QY 586 GAGGACGAGAAATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTGTCTCTCTCTGC 645
DB |||||
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QY 734 AAGTGTGTTGGGGCTACAGGCGCTGTGAGGTGGCCCTTTGCAAAAGCATCTTCCAAAGGA 793
Db 646 AAGGTTTTTCGGCGCCCAACAGGACTGTGAGGTGGCCCTCTGCCACCAATTTACAAAGC 705
QY 794 CAGAAGACTGAGTGAAGTACTGCATCTCCATGCTGTGTGGGGGACGACCGAGTGCAG 853
Db 706 CAGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 765
QY 854 ACATCATCTCTCAGCTGGAGGAGTCTGTCGAGAGTGAACCAAGGAGATAGCCACCAAGGTG 913
Db 766 GCAGTGAATACCCAGATGGAGGAGGTGTGCAGACCAATTCAGAGACACAGCCGACAGAG 825
QY 914 AAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
Db 826 AAGCAACTGTATAACACAGAGGTTCCAGACCCCTGTGCGCGTGTGGAGGAGCGCAAGGGC 885
QY 974 GAGCTCTGACGCGGATCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
Db 886 GAATCTGTTCAAGACTGTGCGCGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
QY 1034 ATCTTCAGTACAGGAGGAGCTGGAAAAAGTCCACCAAGCTTGTGGAGACCGCATCCAG 1093
Db 946 ATCCGACAGTACGAGACCACTTGGAGGCTCTCAAGAGTGTGTGAGTCCGACATCCAG 1005
QY 1094 TCCTGTGATGAGCCGAGGAGGCTACTTCTCTCAAGTGCCCAAGCAGCTCATCAAGAGC 1153
Db 1006 TCCATGAGGAGCGCAGATGGCTCTCTACCTCCAGCAGGCAAGGAGCTGATCAACAG 1065
QY 1154 ATTGTAGAGCTTCCAGGCTCCAGCTGGGAGACAGAGGAGGAGGAGGAGGAGGAGGAGG 1213
Db 1066 GTCGGGCAATGTGCAAGTGTGAGCTGGCAGGACCGCCGAGCCAGGCTATGAGAGCATG 1125
QY 1214 GACTACTTTACTCTGAGCTTAGAACATACATGAGGAGGCTTGTAGGCGCATTTGAGTGGG 1273
Db 1126 GAGCAATCTCTGTAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 1185
QY 1274 ACAGGTAAGAGTGTGATG 1292
Db 1186 CCGGGCGCGCTGGGATG 1204
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RESULT 18

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US-09-890-688-57
; Sequence 57, Application US/09890688
; Publication No. US20030144475A1
; GENERAL INFORMATION:
; APPLICANT: Seishi KATO
; APPLICANT: Chikashi EGUCHI
; APPLICANT: Minoru SAEKI
; TITLE OF INVENTION: Human Proteins and cDNAs thereof
; FILE REFERENCE: 2001-1102A/WMC/00653
; CURRENT APPLICATION NUMBER: US/09/890,688
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: JP 11-346863
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 11-34684
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 2000-31062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34091
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; PRIOR APPLICATION NUMBER: JP 2000-34090
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; PRIOR APPLICATION NUMBER: JP 2000-35899
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-71161
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: JP 2000-160851
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 57
; LENGTH: 1913
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (303)..(1379)
US-09-890-688-57

Query Match          30.2%; Score 481.8; DB 10; Length 1913;
Best Local Similarity 69.4%; Pred. No. 1.1e-141;
Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 317 CTGATTTCTCTGATGGAAACGCTATGGAGAAACCTTGGAGAACGAGCTGATCTGCCCATCTTGC 376
Db 330 CTGCTAGGGGATGTCACACAGCATGGACAACCTTGGAGAACGAGCTCATCTGCCCATCTGC 389
QY 377 CTGGAGATGTTTACCAAGCCTGTGFTCATCTCTGCCCTGCGAACACAACTCTTGCCTGCGAAG 436
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Db 450 TGTGCCAACGACGCTCTTCCAGGCTTCCGAATCTCTTATGGAAGTCTCCGGGGCTCCACCACT 509
QY 497 TCCATGCTGTGGAGGTGTTTCCGTTTCCGCTCGTGGCGCATGAAGTGTATCTGGACCGG 556
Db 510 GTGTCTTTCAGGAGGCGGTTTCCGCTGCCCATGCTGTGAGCATGAGGTTGTCTGGACAGA 569
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QY 674 GAAGACGAGAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTACTTGTCTTGTGTGC 733
Db 690 GAAGAAGAGAGATCAATATTTACTGCTGAGCTGTGAGGTGCCACCTGCTCTCTCTCTGC 749
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QY 1154 ATTGTAGAGGCTTCAAGAGGCTGCCAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1213
Db 1170 GTCGGGGCCATGTTCGAAAGTGGAGTGGCAGGCGCGGAGGAGGAGGAGGAGGAGGAGG 1229
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Db	388	GAAGAAGAGAATCAATATTACTGCTGAGCTGTGAGGTGCCACCTCTCTCTGC	447
Qy	734	AAGGTGTTGGGGCTCACAGGCTGTGAGGTGCCCCCTTTGCCAAGCATCTTCCAAAGGA	793
Db	448	AAGGTCTTCGGTGGCCCAAGGAGCTGTGAGGTGGCCCCACTGCCCCACCAATTACAAAGC	507
Qy	794	CAGAAGACTGAGCTGAGTAACTCATCTCCATCTGCTGGGGGACGACCGAGTGCCAG	853
Db	508	CAGAAGAGTGAGCTCAGCGATGGCATGCGCATGCTGGTGGCAGGCAATGACCGGTGCAA	567
Qy	854	ACGATCATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAAATAGCCACCAAGGTG	913
Db	568	GCAGTGATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACATAGCCCGAGGCAG	627
Qy	914	AAGGAGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTTGATGAGAAAGAGC	973
Db	628	AAGCAGTTGTTAAACCAGAGGTTTGACAGCCTGTGCGCAGTGTGGAGGAGCGCAAGGGT	687
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Qy	1034	ATCCTCCAGTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCATCCAG	1093
Db	748	ATCCGTCAGTATGGCGACCACCTGGAGGCTCTCTTAAGCTGTGGAGTCTGCCATCCAG	807
Qy	1094	TCCCTGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCCCAAGCAGCTCATCAAGA	1151
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